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OM protein - protein search, using sw model

Run on: June 25, 2004, 15:13:28 ; Search time 48 Seconds
(without alignments)
1346.871 Million cell

Title: US-09-856-320A-2 COPY 54 282

Perfect score:

Sequence: 1 IIKGFECKPHSQPWQAALFE.....GVYTKVCKYVDWIQETMKNN 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 702159

Minimum DB seq length: 0

Maximum DB seq length: 229

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Database : Published Applications AA

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	679	54.0		225	12	US-10-072-012-611	Sequence 611, App
2	651	51.7		228	10	US-09-933-767-1150	Sequence 1150, App
3	651	51.7		228	12	US-10-004-860-1150	Sequence 1150, App
4	651	51.7		228	14	US-10-023-282-1150	Sequence 1150, App
5	630.5	50.1		220	9	US-09-739-977-180	Sequence 180, App
6	630.5	50.1		220	11	US-09-938-671-180	Sequence 180, App
7	564	44.8		229	12	US-10-654-823-2	Sequence 2, Appl
8	563	44.8		223	9	US-09-910-071-14	Sequence 14, Appl
9	560.5	44.6		215	10	US-09-898-837A-50	Sequence 50, Appl
10	546	42.4		225	16	US-10-600-187-4	Sequence 4, Appl
11	534	42.4		225	16	US-10-600-187-5	Sequence 5, Appl
12	523.5	41.6		226	14	US-10-312-089-8	Sequence 8, Appl
13	520.5	41.4		220	9	US-09-759-143-327	Sequence 327, App
14	520.5	41.4		220	9	US-09-780-669-327	Sequence 327, App
15	520.5	41.4		220	9	US-09-822-827-327	Sequence 327, App

89	365	29.0	207	14	US-10-154-678-54	Sequence 54, Appl	162	250	19.9	220	14	US-10-131-409-24	Sequence 24, Appl
90	362.5	28.8	166	9	US-09-759-143-838	Sequence 838, App	163	250	19.9	220	15	US-10-150-811-24	Sequence 24, Appl
91	362.5	28.8	166	9	US-09-780-669-838	Sequence 838, App	164	249	19.8	220	15	US-10-150-811-98	Sequence 98, Appl
92	362.5	28.8	166	9	US-09-822-827-838	Sequence 838, App	165	249	19.8	220	15	US-10-139-854-98	Sequence 98, Appl
93	362.5	28.8	166	9	US-09-895-793-838	Sequence 838, App	166	249	19.8	220	15	US-10-131-409-98	Sequence 98, Appl
94	362.5	28.8	166	9	US-09-895-814-838	Sequence 838, App	167	249	19.8	220	15	US-10-150-811-98	Sequence 98, Appl
95	362.5	28.8	166	13	US-10-012-896-838	Sequence 838, App	168	241.5	19.2	220	15	US-10-357-175-22	Sequence 22, Appl
96	362.5	28.8	166	14	US-10-144-678A-838	Sequence 838, App	169	241.5	19.2	220	15	US-10-455-720-22	Sequence 22, Appl
97	362.5	28.8	166	14	US-10-294-035-838	Sequence 838, App	170	236.5	18.8	220	15	US-09-888-615-93	Sequence 93, Appl
98	361.5	28.7	228	15	US-10-156-214A-272	Sequence 272, App	171	232.5	18.5	220	15	US-10-074-978A-220	Sequence 220, App
99	361	28.7	151	14	US-10-357-175-21	Sequence 21, Appl	172	231	18.4	220	15	US-09-910-151-4	Sequence 4, Appl
100	361	28.7	151	15	US-10-455-720-21	Sequence 21, Appl	173	231	18.4	220	15	US-10-174-333-157	Sequence 157, App
101	360.5	28.7	228	14	US-10-203-676-6	Sequence 6, Appl	174	225	17.9	200	12	US-10-150-811-96	Sequence 96, Appl
102	360	28.6	159	9	US-09-759-143-172	Sequence 172, App	175	224	17.8	197	12	US-10-139-854-96	Sequence 96, Appl
103	360	28.6	159	9	US-09-780-669-172	Sequence 172, App	176	224	17.8	197	12	US-10-131-409-96	Sequence 96, Appl
104	360	28.6	159	9	US-09-030-606-172	Sequence 172, App	177	224	17.8	197	15	US-10-150-811-96	Sequence 96, Appl
105	360	28.6	159	9	US-09-822-827-172	Sequence 172, App	178	220	17.5	159	14	US-10-357-175-24	Sequence 24, Appl
106	360	28.6	159	9	US-09-115-453-172	Sequence 172, App	179	220	17.5	159	15	US-10-455-720-24	Sequence 24, Appl
107	360	28.6	159	9	US-09-232-880-172	Sequence 172, App	180	218.5	17.4	164	9	US-09-759-143-178	Sequence 178, App
108	360	28.6	159	9	US-09-895-793-172	Sequence 172, App	181	218.5	17.4	164	9	US-09-780-669-178	Sequence 178, App
109	360	28.6	159	9	US-09-895-814-172	Sequence 172, App	182	218.5	17.4	164	9	US-09-030-606-178	Sequence 178, App
110	360	28.6	159	13	US-10-012-896-172	Sequence 172, App	183	218.5	17.4	164	9	US-09-822-827-178	Sequence 178, App
111	360	28.6	159	14	US-10-010-940-172	Sequence 172, App	184	218.5	17.4	164	9	US-09-115-453-178	Sequence 178, App
112	360	28.6	159	14	US-10-144-678A-172	Sequence 172, App	185	218.5	17.4	164	9	US-09-232-880-178	Sequence 178, App
113	360	28.6	159	14	US-10-294-025-172	Sequence 172, App	186	218.5	17.4	164	9	US-09-895-793-178	Sequence 178, App
114	349	27.7	161	12	US-10-344-394-8	Sequence 8, Appl	187	218.5	17.4	164	9	US-09-895-814-178	Sequence 178, App
115	344.5	27.4	133	15	US-10-264-049-3307	Sequence 3307, Ap	188	218.5	17.4	164	13	US-10-012-896-178	Sequence 178, App
116	339.5	27.0	224	9	US-09-815-876-4	Sequence 4, Appl	189	218.5	17.4	164	14	US-10-010-940-178	Sequence 178, App
117	339	26.9	144	9	US-09-796-294-1	Sequence 1, Appl	190	218.5	17.4	164	14	US-10-144-678A-178	Sequence 178, App
118	339	26.9	144	14	US-10-461-787-1	Sequence 1, Appl	191	218.5	17.4	164	14	US-10-357-175-25	Sequence 25, Appl
119	339	26.9	146	9	US-09-796-294-3	Sequence 3, Appl	192	218.5	17.4	164	14	US-10-294-025-178	Sequence 25, Appl
120	339	26.9	146	14	US-10-461-787-3	Sequence 3, Appl	193	218.5	17.4	164	15	US-10-455-720-25	Sequence 25, Appl
121	338.5	26.9	229	10	US-09-898-837A-53	Sequence 53, Appl	194	216.5	17.2	203	15	US-10-074-566-118	Sequence 118, App
122	327	26.0	119	12	US-10-262-511-54	Sequence 54, Appl	195	215.5	17.1	154	14	US-10-029-386-32241	Sequence 32241, A
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124	327	26.0	148	12	US-10-262-511-58	Sequence 52, Appl	197	214	16.9	157	15	US-10-455-720-23	Sequence 39, Appl
125	325.5	25.9	102	12	US-10-262-511-56	Sequence 56, Appl	198	214	16.9	157	15	US-09-997-003-39	Sequence 39, Appl
126	320	25.4	224	16	US-10-408-765A-345	Sequence 345, App	199	204.5	16.3	192	9	US-09-935-297-529	Sequence 529, App
127	319	25.4	144	9	US-09-796-294-4	Sequence 4, Appl	200	203.5	16.2	135	14	US-10-148-671-24	Sequence 24, Appl
128	319	25.4	144	14	US-10-461-787-4	Sequence 4, Appl	201	202	16.1	222	9	US-09-832-197-5	Sequence 5, Appl
129	316.5	25.2	119	12	US-10-262-511-60	Sequence 60, Appl	202	202	16.1	222	14	US-10-162-742-5	Sequence 5, Appl
130	315.5	25.1	286	16	US-10-408-765A-353	Sequence 353, App	203	200	15.9	228	14	US-10-174-333-107	Sequence 107, App
131	303.5	24.1	140	12	US-10-247-703-18	Sequence 18, App	204	199	15.8	98	14	US-10-240-730-2	Sequence 2, Appl
132	295.5	23.5	163	16	US-10-408-765A-2795	Sequence 2795, Ap	205	198.5	15.8	159	14	US-09-796-294-5	Sequence 5, Appl
133	295.5	23.5	176	12	US-10-247-703-12	Sequence 12, Appl	206	198	15.7	159	14	US-10-461-787-5	Sequence 5, Appl
134	295.5	23.5	176	12	US-10-247-703-14	Sequence 14, Appl	207	198	15.7	159	14	US-10-462-511-50	Sequence 50, Appl
135	295.5	23.5	180	15	US-10-341-434-36	Sequence 36, Appl	208	195.5	15.5	187	9	US-09-804-156-17	Sequence 17, Appl
136	294.5	23.4	144	10	US-09-860-739-2	Sequence 2, Appl	209	195.5	15.5	187	13	US-10-125-459-9	Sequence 9, Appl
137	293.5	23.3	182	12	US-10-307-817-148	Sequence 148, App	210	195.5	15.5	187	13	US-10-067-761-17	Sequence 17, Appl
138	285	22.7	181	9	US-09-864-761-46600	Sequence 46600, A	211	195.5	15.5	187	13	US-10-319-519-17	Sequence 17, Appl
139	284.5	22.6	222	15	US-10-423-311-1	Sequence 1, Appl	212	195.5	15.5	187	14	US-10-262-511-58	Sequence 2, Appl
140	281.5	22.4	206	10	US-09-898-837A-42	Sequence 42, Appl	213	194	15.4	217	9	US-09-755-016-2	Sequence 2, Appl
141	278	22.1	121	14	US-10-344-394-7	Sequence 7, Appl	214	193.5	15.4	164	9	US-09-735-713A-6	Sequence 5, Appl
142	276.5	22.0	169	14	US-10-106-698-6322	Sequence 6322, Ap	215	184.5	14.7	164	10	US-09-860-739-5	Sequence 80, Appl
143	276.5	22.0	227	9	US-09-868-615-84	Sequence 84, Appl	216	184	14.6	54	10	US-10-316-253-80	Sequence 100, App
144	268.5	21.3	193	12	US-10-243-552-890	Sequence 890, App	217	182	14.5	66	14	US-10-262-511-100	Sequence 155, App
145	266.5	21.2	217	14	US-10-106-698-4740	Sequence 4740, Ap	218	179	14.2	97	12	US-10-174-333-155	Sequence 4, Appl
146	257	20.4	133	9	US-09-925-297-642	Sequence 642, App	219	177.5	14.1	217	14	US-10-376-345-4	Sequence 4, Appl
147	256.5	20.4	218	9	US-09-861-708-3	Sequence 3, Appl	220	177	14.1	217	14	US-10-376-345-6	Sequence 6, Appl
148	255.5	20.3	227	16	US-10-275-505-7	Sequence 7, Appl	221	177	14.1	217	14	US-09-759-143-329	Sequence 329, App
149	254.5	20.2	199	14	US-10-384-474-8	Sequence 8, Appl	222	174	13.8	77	9	US-09-780-669-329	Sequence 329, App
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151	253.5	20.2	218	16	US-10-408-765A-87	Sequence 87, Appl	224	174	13.8	77	9	US-09-232-880-329	Sequence 329, App
152	250	19.9	203	12	US-10-150-813-95	Sequence 95, Appl	225	174	13.8	77	9	US-09-895-793-329	Sequence 329, App
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159	250	19.9	205	15	US-10-150-811-97	Sequence 97, Appl	232	170.5	13.6	130	12	US-10-174-333-177	Sequence 18, Appl
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161	250	19.9	220	12	US-10-139-854-24	Sequence 24, Appl	234	169	13.4	219	13	US-10-067-761-18	Sequence 18, Appl

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236	168	13.2	120	14	US-10-332-122-4	Sequence 4, Appl	309	95	7.6	35	9	US-09-885-441-3	Sequence 3, Appl
237	165.5	13.4	116	12	US-10-424-599-236797	Sequence 436797, A	310	95	7.6	35	12	US-10-424-836-3	Sequence 3, Appl
238	165	13.1	223	15	US-10-108-260A-4500	Sequence 4500, Ap	311	95	7.6	56	9	US-09-864-761-44838	Sequence 44838, A
239	156.5	12.4	97	12	US-09-825-751A-8	Sequence 8, Appl	312	95	7.6	56	9	US-09-864-761-45193	Sequence 45193, A
240	152.5	12.1	140	12	US-10-424-599-157545	Sequence 157545, A	313	93	7.4	38	9	US-09-910-151-9	Sequence 9, Appl
241	148.5	11.8	183	12	US-10-424-599-263901	Sequence 263901, A	314	92.5	7.4	90	15	US-10-074-566-119	Sequence 119, App
242	147	11.7	80	12	US-10-296-115-1294	Sequence 1294, Ap	315	92.5	7.4	90	15	US-10-074-566-120	Sequence 120, App
243	146.5	11.6	148	15	US-10-074-978A-216	Sequence 216, App	316	92	7.3	44	12	US-09-826-734-72	Sequence 72, Appl
244	146.5	11.6	200	12	US-09-968-415-5	Sequence 5, Appl	317	91.5	7.3	213	9	US-09-826-734-72	Sequence 72, Appl
245	145.5	11.6	200	14	US-10-180-719-5	Sequence 5, Appl	318	90.5	7.2	72	12	US-10-424-599-210705	Sequence 210705, A
246	145.5	11.4	213	15	US-10-004-378A-146	Sequence 146, App	319	89.5	7.1	38	9	US-09-879-792-18	Sequence 18, Appl
247	143.5	11.4	52	9	US-09-832-197-7	Sequence 7, Appl	320	88	7.0	30	9	US-09-820-893-11	Sequence 11, App
248	143.5	11.3	52	14	US-10-162-742-7	Sequence 7, Appl	321	88	7.0	30	12	US-10-607-565-111	Sequence 11, App
249	142.5	11.3	81	13	US-10-045-367A-7	Sequence 7, Appl	322	88	7.0	48	9	US-09-910-151-8	Sequence 8, Appl
250	142.5	11.3	81	14	US-10-170-789-57	Sequence 57, Appl	323	87	6.9	45	9	US-09-888-615-116	Sequence 116, App
251	142.5	11.3	130	15	US-10-291-265-714	Sequence 714, App	324	86.5	6.9	35	9	US-10-424-836-8	Sequence 8, Appl
252	138.5	11.0	49	14	US-10-029-386-1646	Sequence 1646, A	325	86.5	6.9	35	12	US-10-424-836-8	Sequence 8, Appl
253	136	10.8	196	9	US-09-764-898-134	Sequence 194, App	326	85.5	6.8	29	9	US-09-826-734-72	Sequence 72, Appl
254	136	10.8	196	9	US-09-764-898-267	Sequence 267, App	327	84.5	6.7	125	12	US-10-276-774-2659	Sequence 2659, Ap
255	135.5	10.8	146	10	US-09-925-297-643	Sequence 643, App	328	84	6.7	72	9	US-09-864-761-35323	Sequence 35323, A
256	135.5	10.8	146	9	US-09-925-297-643	Sequence 643, App	329	84	6.7	225	9	US-09-764-898-227	Sequence 227, App
257	133	10.6	156	12	US-10-424-599-149734	Sequence 149734, A	330	84	6.7	225	10	US-09-989-442-131	Sequence 131, App
258	131.5	10.5	78	11	US-09-864-408A-608	Sequence 608, App	331	81.5	6.5	35	16	US-10-297-987B-23	Sequence 23, Appl
259	131	10.4	79	14	US-10-029-386-29504	Sequence 29504, A	332	81.5	6.5	224	12	US-10-424-599-268213	Sequence 268213, A
260	131	10.4	113	14	US-10-029-386-31617	Sequence 31617, A	333	81	6.4	15	14	US-10-144-678A-1032	Sequence 1032, Ap
261	129	10.3	224	15	US-10-074-566-43	Sequence 43, Appl	334	81	6.4	15	14	US-10-294-025-1032	Sequence 1032, Ap
262	128	10.2	189	15	US-10-074-566-66	Sequence 66, Appl	335	81	6.4	15	14	US-10-045-170A-16	Sequence 16, Appl
263	128	10.2	189	15	US-10-074-566-74	Sequence 74, Appl	336	81	6.4	18	14	US-10-044-708A-29	Sequence 29, App
264	128	10.2	198	13	US-10-000-512-16	Sequence 16, Appl	337	80	6.4	18	9	US-09-826-290-247	Sequence 247, App
265	128	10.2	198	15	US-10-074-566-16	Sequence 16, Appl	338	80	6.4	18	16	US-10-264-309-68	Sequence 68, Appl
266	126.5	10.1	101	9	US-09-925-299-1243	Sequence 1243, Ap	339	80	6.4	30	9	US-09-820-893-110	Sequence 110, App
267	126.5	10.1	101	10	US-09-925-299-1243	Sequence 1243, Ap	340	80	6.4	30	12	US-10-607-565-110	Sequence 110, App
268	125	9.9	166	9	US-09-925-299-1177	Sequence 1177, Ap	341	79	6.3	17	16	US-10-297-987B-14	Sequence 14, Appl
269	125	9.9	166	14	US-09-925-299-1177	Sequence 1177, Ap	342	79	6.3	18	16	US-10-297-987B-13	Sequence 13, Appl
270	122.5	9.7	184	14	US-10-029-386-33844	Sequence 33844, A	343	79	6.3	27	14	US-10-128-965-36	Sequence 36, Appl
271	121	9.6	124	14	US-10-357-175-157	Sequence 157, App	344	78.5	6.2	188	9	US-09-779-323-1	Sequence 1, Appl
272	120	9.5	44	9	US-09-910-151-7	Sequence 7, Appl	345	78.5	6.2	31	12	US-10-071-214-12	Sequence 12, Appl
273	117	9.3	60	14	US-10-094-507-22	Sequence 22, Appl	346	77.5	6.2	23	9	US-09-879-792-22	Sequence 22, Appl
274	115	9.1	53	9	US-09-864-761-44996	Sequence 44996, A	347	77.5	6.2	159	15	US-10-108-260A-2919	Sequence 2919, Ap
275	115	9.1	118	15	US-10-104-047-3004	Sequence 3004, A	348	77	6.1	23	14	US-10-044-708A-30	Sequence 30, Appl
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277	113.5	9.0	172	9	US-09-764-898-328	Sequence 328, App	350	76	6.0	31	12	US-10-071-214-13	Sequence 13, Appl
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ALIGNMENTS

RESULT 1

US-10-072-012-611
; Sequence 611, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Fatturajan, Meera
; APPLICANT: Shamkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.

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; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
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; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 611
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-072-012-611

Query Match      54.0%; Score 679; DB 12; Length 225;
Best Local Similarity 53.1%; Pred. No. 3.5e-60;
Matches 120; Conservative 35; Mismatches 69; Indels 2; Gaps 2;

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RESULT 2
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; Sequence 1150, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 05/205,258
; PRIOR FILING DATE: 1998-12-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1150
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-1150

```

```

Query Match      51.7%; Score 651; DB 10; Length 228;
Best Local Similarity 91.7%; Pred. No. 2.4e-57;
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 1 IIKGFECKPHSQPQQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
Db 4 IIKGFECKLHSQPQQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 63

Qy 61 GCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTAAGTS 120
Db 64 GCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTAAGTS 123

Qy 121 CLISGWGSTSSP 132
Db 124 CSFPAGARPD 135

```

```

RESULT 3
US-10-004-860-1150
; Sequence 1150, Application US/10004860
; Publication No. US20030065160A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; PRIOR FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0

```

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; SEQ ID NO 1150
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-004-860-1150

Query Match      51.7%; Score 651; DB 12; Length 228;
Best Local Similarity 91.7%; Pred. No. 2.4e-57;
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 1 IIKGFECKPHSQPQQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
Db 4 IIKGFECKLHSQPQQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 63

Qy 61 GCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTAAGTS 120
Db 64 GCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTAAGTS 123

Qy 121 CLISGWGSTSSP 132
Db 124 CSFPAGARPD 135

```

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RESULT 4
US-10-023-282-1150
; Sequence 1150, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06

```

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; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1150
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-1150

Query Match      51.7%; Score 651; DB 14; Length 228;
Best Local Similarity 91.7%; Pred. No. 2,4e-57;
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 IIKGFCEKPHSQPQQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLOKEE 60
Db 4 IIKGFCEKLSQPQQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLOKEE 63
QY 61 GCEQRTATESPPHGFNNLSLNKDHNDIMLVKVASPVSIWAVRPLTSSRCVTAGTS 120
Db 64 GCEQRTATESPPHGFNNLSLNKDHNDIMLVKVASPVSIWAVRPLTSSRCVTAGTS 123
QY 121 CLISWGSTSSP 132
Db 124 CSFPAGAARPD 135

RESULT 5
US-09-739-907-180
; Sequence 180, Application US/09739907
; Patent No. US20010012889A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

Query Match      50.1%; Score 630.5; DB 11; Length 220;
Best Local Similarity 50.7%; Pred. No. 2.7e-55;
Matches 114; Conservative 39; Mismatches 65; Indels 7; Gaps 4;

; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2022P1
; CURRENT APPLICATION NUMBER: US/09/739,907
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/348,457
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; PRIOR FILING DATE: 1998-01-07
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-739-907-180
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; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2022P1
; CURRENT APPLICATION NUMBER: US/09/739,907
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/348,457
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; PRIOR FILING DATE: 1998-01-07
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-739-907-180

Query Match      50.1%; Score 630.5; DB 9; Length 220;
Best Local Similarity 50.7%; Pred. No. 2.7e-55;
Matches 114; Conservative 39; Mismatches 65; Indels 7; Gaps 4;

QY 7 CKPHSQPQQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLOK-EEGCEQ 64
Db 1 CDVHTQPQQAALLRPNQLYCGAVLVHPQWLLTAACHCKKVRVRLGHVLSLPYESGQQ 60
QY 65 TRTATESPPHGFNNLSLNKDHNDIMLVKVASPVSIWAVRPLTSSRCVTAGTSCLIS 124
Db 61 MFCGVKSIPIHFGYS----HFGHNDLMLIKLNRIIPTKDVREINVSCHSPSAGTKCLVS 116
QY 125 GWGSTSPQLRPLHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKDCQGDSSG 184
Db 117 GWGTTKSPQVHPKVLQCLNISVLSQKCEDAIPRQIDDTMFAG-DKAGRDSQQDSSG 175
QY 185 PLVGNQSLQIISWGQDPQCAITRKPGYIVTKYKVDWIQETMKN 229
Db 176 PVVNGSLQGLVSWGDPYPCARNRPGYVITNLCKFTKWIQETIQAN 220

RESULT 6
US-09-938-671-180
; Sequence 180, Application US/09938671
; Publication No. US20040002066A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2022P1
; CURRENT APPLICATION NUMBER: US/09/938,671
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/348,457
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; PRIOR FILING DATE: 1998-01-07
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-671-180

Query Match      50.1%; Score 630.5; DB 11; Length 220;
Best Local Similarity 50.7%; Pred. No. 2.7e-55;
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	Matches	114;	Conservative	39;	Mismatches	65;	Indels	7;	Gaps	4;
QY	7	KXPHSQWAA-LPEKTRLLCGATLIAPRWLLTAACHCLKPRYIVHIGHQNLQK-EEGCEQ	64							
Db	1	CDMHTQWQAALLRPNPQLYCGAVLHPQWLLTAACHCKKVFVRVRLGHVYLSPPVYESQQ	60							
QY	65	TRTATESPPHGFNNSLPNKDHRNDIMLVKASFSVITWAVRPLTLSSRCVTAGTSCILS	124							
Db	61	MEQGVKSIPIHPGYS----HPGSHNDLMLIKLNRIRPTKDVRPINVSCHPSAGTKCLVS	116							
QY	125	GWGTSSTSQLALPHTLRGANITIEHCKCKENAYPGNITDTWCASVQEGGKDSCGDGGG	184							
Db	117	GWGITKSPQVHPKVKQLCNLSVQKRCEDNAIPRQIDDTMFCAG-DXAGRDSQQGDSGG	175							
QY	185	PLVNCISQGGIISWGQDFCAITRPGVYTKVCKYVDWIQETMKN	229							
Db	176	PWVNCGISQGLVSGMDYPCARPNEPQVYTNLCFTKWIQETIOAN	220							

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RESULT 7
US-10-654-823-2
; Sequence 2, Application US/10654823
; Publication No. US20040049812A1
; GENERAL INFORMATION:
; APPLICANT: Howard, John A.
; APPLICANT: Hood, Elizabeth
; TITLE OF INVENTION: COMMERCIAL PRODUCTION OF PROTEASES IN PLANTS
; FILE REFERENCE: 10014
; CURRENT APPLICATION NUMBER: US/10/654,823
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/120,582
; PRIOR FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 2
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-654-823-2

Query Match 44.8%; Score 564; DB 12; Length 229;
Best Local Similarity 46.7%; Pred. No. 1.Se-48;
Matches 107; Conservative 38; Mismatches 78; Indels 6; Gaps 3;

Qy 1 I I K G F E C K P H S Q P W Q A A L F E K T R L L C G A T L I A P R W L L I T A A H C L K P R Y I V H L G O H N L Q K E E 60
Db 7 I V G Y T C G A N T V P Q V S L - N S G Y H F C G S L I N S Q W V V S A A H C Y K S G I Q V R L G E D N I N V V E 65

Qy 61 G C Q T R T A T S F P H P G P N S L P N K D H N D I M L V K M A S P V S I T W A V R P L T L S S R C V T A G T S 120
Db 66 G N E Q F T S A S K S I V H P S Y N S T L N - - - - N D M L I K L K S A A S L N S R V A S I S L P T S C A S A G T Q 121

Qy 121 C L I S G M G S T S P Q L R L P H T L R C A N I T I E H O K E N A Y P G N I T D T M V C A S V O E G G K D S C Q G 180
Db 122 C L I S G W G T S S G T S Y D V L K L C A P I L S D S S C K S A Y P G Q I T S N M F C A G V L E G G K D S C Q G 181

Qy 181 D S G G P L V C N S L Q G I I S W G D P C A I T R K P G V Y T K V K Y V D W I O E T M K Q N 229
Db 182 D S G G P V V C S G K L Q G I V S W G S G - C A Q K N K P G V Y T K V C N V S W I K Q T I A S N 229

RESULT 8
US-09-910-071-14
; Sequence 14, Application US/09910071
; Patent No. US20020116146A1
; GENERAL INFORMATION:
; APPLICANT: Tomikawa, Mayumi
; APPLICANT: Aikawa, Seiichi
; APPLICANT: Matsuzawa, Fumiko
; TITLE OF INVENTION: Method and Apparatus for Extracting and Evaluating Mutually Similar
; TITLE OF INVENTION: Portions in One-Dimensional Sequences in Molecules and/or Three
; TITLE OF INVENTION: Structures of Molecules
; FILE REFERENCE: 522.1921D2

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; CURRENT APPLICATION NUMBER: US/09/910,071
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/014,867
; PRIOR FILING DATE: 1993-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 223
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: amino acid sequence of tryptsin
US-09-910-071-14

Query Match 44.8%; Score 563; DB 9; Length 223;
Best Local Similarity 46.7%; Pred. No. 1.8e-48;
Matches 107; Conservative 38; Mismatches 78; Indels 6; Gaps 3

QY 1 IIKGPECKPHSQPQQAALFEKRLLOGATIIAPRWLLTAHCLKPRYIVHLGCHNLQKEE 60
Db 1 IVGGYTCCANTVPYQVSL-NSGYHFCGSLNSQWVYSAHCYKSGIQVRLGEDINVVE 59
QY 61 GCEQRTATESPFPHPGFNNSLPNKHENDIMLVKMAASPVYSITWAVRPLTLSSRCVTAGTS 120
Db 60 GNEQFISAKSIVHPFSYNSNTLN----NDIMLVKLSAASLNSRVSASILPSCASAGTQ 115
QY 121 CLISGWGTSSTSPQRLPHLTLBCANITIIHQKENAYPNGITDTMVCASVOEGKDCSCG 180
Db 116 CLISGWGNTKSGTSPYDLVKLKPAILSDSSCKSAYPGGIITSNMFCAGYLEGDKDCSCG 175
QY 181 DSGGPLVNCQSLQIHSWGDPFCATIRKPGVYTKVKYVDWIQETMKN 229
Db 176 DSGGPGVCSGKLGIVSNGSG-CACKNKPGYTKVCNVSWIKQTIAN 223

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RESULT 9
US-09-898-837A-50
; Sequence 50, Application US/09898837A
; Publication NO. US20030077697A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Herrmann, John L.
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Rastelli, Luca
; APPLICANT: Curagen Corporation
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 15966-598 CIP
; CURRENT APPLICATION NUMBER: US/09/898,837A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,985
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
; PRIOR FILING DATE: 2000-07-03


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; SEQ ID NO 8
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-312-089-8

Query Match          41.6%; Score 523.5; DB 14; Length 226;
Best Local Similarity 42.2%; Pred. No. 1.8e-44;
Matches 95; Conservative 47; Mismatches 76; Indels 7; Gaps 3;

QY 4 GFCEKPSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGC 62
DB 6 GEDCSPHSQWQAALVMEENELFCGVLVHPQWVLSAAHCFQNSYITGLGHSLEADQEPG 65
QY 63 EQRTATESPPHGFNNSLPNKDRNDIMLVKASPVISITWAVRPLTLSSRCVTAGTSC 122
DB 66 SQMVEASLSVRHPEYRNP-----LANDMLIKLDESVSSESDTIRSIASQCPTAGNSCL 121
QY 123 ISGWSTSSPOLRPLPHTLRCAITIEHOKCENAYPGNITDTMVCASVQEGGKDCSQGDS 182
DB 122 VSGWGLLANG--RMPVLQCVNVSVVSEVCSKLYDPLVHPSMFCAGGQDQKDCSNGDS 179
QY 183 GGPLVNCQSLOGIISWGQDPCAIRKPGVYTKVCKYVDWMIQETMK 227
DB 180 GGPLICNGYLQGLVSPGKAPCGQGVPGVYTNLCKFTWIEKTVQ 224

RESULT 13
US-09-759-143-327
; Sequence 327, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-327

Query Match          41.4%; Score 520.5; DB 9; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQWQAALVMEENELFCGVLVHPQWVLSAAHCFQNSYITGLGHSLEADQEPG 61
QY 65 TRTATESPPHGFNNSLPNKDRNDIMLVKASPVISITWAVRPLTLSSRCVTAGTSC 124
DB 62 MVEASLSVRHPEYRNP-----LANDMLIKLDESVSSESDTIRSIASQCPTAGNSCL 117
QY 125 GWSSTSSPOLRPLPHTLRCAITIEHOKCENAYPGNITDTMVCASVQEGGKDCSQGDS 184
DB 118 GWGLLANG--RMPVLQCVNVSVVSEVCSKLYDPLVHPSMFCAGGQDQKDCSNGDS 175
QY 185 PLVNCQSLOGIISWGQDPCAIRKPGVYTKVCKYVDWMIQETMK 227
DB 176 PLICNGYLQGLVSPGKAPCGQGVPGVYTNLCKFTWIEKTVQ 218

RESULT 15
US-09-822-827-327
; Sequence 327, Application US/09822827
; Patent No. US20020081680A1

Query Match          41.4%; Score 520.5; DB 9; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQWQAALVMEENELFCGVLVHPQWVLSAAHCFQNSYITGLGHSLEADQEPG 61
QY 65 TRTATESPPHGFNNSLPNKDRNDIMLVKASPVISITWAVRPLTLSSRCVTAGTSC 124
DB 62 MVEASLSVRHPEYRNP-----LANDMLIKLDESVSSESDTIRSIASQCPTAGNSCL 117
```

```

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOURCE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-822-827-327

Query Match 41.4%; Score 520.5; DB 9; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3

QY 6 ECKPHSQPWOAALPEKTKTLLCGATLIAPRWLLTAHCLKPKRYIVHI:QGINLQ-KKEGCBQ 64
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 2 DCSPHSQPWOAALVNNELFCGVLVHPQWVLSSAHCFOQNSYTI:GLGSLSEADQEPGSG 61
QY 65 TATATSPFPHGPFNNLSLENKOHNDIMLVKMAKSPVSTIWA:VRPLTILSSRCVTA:GTSCLIS 124
Db 62 MVEASLSVRHPEYRNP:---LANDLMLIKLDESVSBSDT:IRSISIASQCP:TAGNSCLIVS 117
QY 125 GWSGTSSPQLRLPHLTRCANTITIEHOKENAYPGNITD:TMVCASVQBGGKESCOGDSGG 184
Db 118 GUGLJLJANG--RNPTVLQCVNVSVSEECVKSLYDPLVHP:SNFCAGGGQOQKDCN:GDSGG 175
QY 185 PLVNCNOSLQGISWGQDP:CA:TRKPGVYTVKCYVDW:IQETMK 227
Db 176 PLICNGY:QLGLVSFGKAPCGGVGPGVYTVNLCKFT:EMIEKTQ 218

```

```

RESULT 16
US-09-232-880-327
/ Sequence 327, Application US/09232880
/ Publication No. US20020182596A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
/ TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.428C6
/ CURRENT APPLICATION NUMBER: US/09/232,880
/ CURRENT FILING DATE: 1999-01-15
/ NUMBER OF SEQ ID NOS: 338
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 327
/ LENGTH: 220
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-09-232-880-327

```

Query Match	41.4%	Score 520.5	DB 9	Length 220
Best Local Similarity	42.2%	Pred. No. 3.4e-44		
Matches	94	Conservative	47	Mismatches 75; Indels 7; Gaps 3
QY	6	ECKPHSQPQQAALPEKTRLLCGATLIAPRMLTAAHCLKPRYIVHGLQHNIQ	KEEGCEQ	64
Db	2	DCSPHSQPQQAALVMENELFCGVLVHPQWVLSAAHCFQNSYITIGLGLHSLSEADQEP	QSQ	61
QY	65	TRTATSPFPHGFNNSLNPKHRNDIMLVKASPVSIITWAVRPLTLLSSRCVITAGTSC	SLIS	124
Db	62	MVEASLSVRHPEYNRPL---LANDLMLIKLDESVSSEDITRSISIASQCPAGNSCL	VS	117
QY	125	GGSTSSSPQLRLPHYLRCANITIEHOKCENAVPGNITDPMVCASVQEGGKSCQGD	SGG	184
Db	118	GGGLIANG--RMPVLQCVNYSVVEEVCYSKLDPYHPSMFCAGGGQDQKSCN	GDSSG	175

```

Qy      185 PLVNCOSLQIISWGQPDCAITRKPGVYTKVKCVDWIQETMK 227
       |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      176 PLICNGVLOGLVSGKAPCGGVGVPGYTNLCKFTEWIEKTQV 218

RESULT 17
US-09-895-793-327
; Sequence 327, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-793-327

```

Query Match	41.4%;	Score	520.5;	DB	9;	Length	220;
Best Local Similarity	42.3%;	Pred. No.	3.4e-44;				
Matches	94;	Conservative	47;	Mismatches	75;	Indels	7;
Gaps	3;						
Qy	6	ECKPHSQWAAALFEKTRLCGATLIAPRMLLTAACHLKPRYIVHIGQHNLO-KEEGCEQ	64				
Db	2	DCSFHSQPWQAALWMENELFCSGVLVHPQWLSAAHCFQNSYITIGLGLHSLAEADQEPGSG	61				
Qy	65	TRTATESFPHPGPNNSLPKNDHRNDIMLVKMGAPVSIWAVRPLTSSRCVYTAGTSCSLIS	124				
Db	62	MVEASLSVRHPEYNRPL----LANDMLIKLDSVSSESDTIRSIASQCPAGNSCLVS	117				
Qy	125	GWGSTSPQLRLDHLTRCANITIEHOKCENAVPGNITDTMVCASVOEGKDKCQGSQGG	184				
Db	118	GWGILLANG--RMTVLQCVNVSVEVCSKLYDPLVHPMFCAGGQDQKSCNVDGG	175				
Qy	185	PLVCNOSLQIISWGQDPCAITRKPGYITVKCYVDWIQETMK	227				
Db	176	PLICNGYLOGLVFGFRAPCCQGVPGVYTNLCKFTIEWIKTVO	218				

RESULT 18
US-09-895-814-327
; Sequence 327, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

```

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

```

```

; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-814-327

Query Match 41.4%; Score 520.5; DB 9; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQPQAAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQPQAAALVWENELFCGVLVHPQVLSAHCQNSYITGLGHSLEADQEPGSG 61
QY 65 TRTATESPFPHPFNNSLPNDKDRNDIMLVKMASPVISITWAVRPLTLSSRCVTAGTSC LIS 124
DB 62 MVEASLSVRHPEYNRPL----LANDLMLIKLDESVSSESDTIRISIASQCPTAGNSCLVS 117
QY 125 GWGSTSPQLRPHLTRCANITIEHOKCENAYPGNITDTMVCASVQEGGKDCSGDSGG 184
DB 118 GWGLLANG--RMPTVLQCVNVSVSEVCSKLYDPLVHPNMFACGGQDQKDCSGDSGG 175
QY 185 PLVCNOSLQIISWGQDPCAITRKPGVYTKVKYVDMIQETMK 227
DB 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCKFTWIEKTIVQ 218

```

RESULT 19

```

US-10-012-896-327
; Sequence 327, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

```

```

; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-327

Query Match 41.4%; Score 520.5; DB 13; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQPQAAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQPQAAALVWENELFCGVLVHPQVLSAHCQNSYITGLGHSLEADQEPGSG 61
QY 65 TRTATESPFPHPFNNSLPNDKDRNDIMLVKMASPVISITWAVRPLTLSSRCVTAGTSC LIS 124
DB 62 MVEASLSVRHPEYNRPL----LANDLMLIKLDESVSSESDTIRISIASQCPTAGNSCLVS 117
QY 125 GWGSTSPQLRPHLTRCANITIEHOKCENAYPGNITDTMVCASVQEGGKDCSGDSGG 184
DB 118 GWGLLANG--RMPTVLQCVNVSVSEVCSKLYDPLVHPNMFACGGQDQKDCSGDSGG 175
QY 185 PLVCNOSLQIISWGQDPCAITRKPGVYTKVKYVDMIQETMK 227
DB 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCKFTWIEKTIVQ 218

```

RESULT 20

```

US-10-010-940-327
; Sequence 327, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-010-940-327

```

```

Query Match          41.4%; Score 520.5; DB 14; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY      6  ECKPSQPQAAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNIQ-KEEGCEQ 64
      : ||||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      2  DCSFISQPQAAALWENELFCGVLVHPQWVLNAAHCFQNSYTIIGLGLHSLBADQPSGQ 61
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY     65  TRTATSPFPHGFNNNSLENKORNDIMLVKVASPVSIITMAVRPLTILSSRCVTAGTSCLTIS 124
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db     62  MVEASLSVRHPPEYNRPL---LANDLMLIKLDESVSSEDIRISISIASQCPTAGNSCLVS 117
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY     125  GNGSTSSFPOLRPLPHLRICANITIEHQKCEINAYPGNTITDMVCASVQEGGKSCCGDGGG 184
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db     118  GMLGLANG--RMPTVLQCVNVSVEEVCSKLYDPLVHPSPFCAGGQDQKDCSCNGDGGG 175
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY     185  PLVNCNOSLQIGISWGQDPCAIRKPRGVYTKVCKVDWIQETMK 227
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db     176  PLICNGYLQGLVYFQKAPCGQGVPGVYTNLCRTEWIEKTVQ 218
      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 21
US-10-144-678A-327
; Sequence 327, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-327

```

Query Match	41.14%	Score 520.5	DB 14	Length 220	
Best Local Similarity	42.2%	Pred. No. 3.4e-44			
Matches	94	Conservative 47	Mismatches 75	Indels 7	Gaps 3
QY	6	ECKPHSQWQAALPEKTELLCGATLIAPMLLTAAHCLKPRIVHIGQHNLO-KSEGCQ	64		
Db	2	DCSPHSQWQAALVMENELFCGIVHVPQWVLSAAHCFQNSYTIIGLHLSRADQPSQ	61		
QY	65	TTATATESPPHGFNNLSLNNKDRNDIMLVKAGSPVITWAVRELTLSRCVTVAGTSCHLS	124		

Db	62	MVEASLSVRHPEYNRPL-----LANDMLMLIKLDESVSSEDTIRSIASQCFTAGNSCLVS	117
Qy	125	GWGSTSSPQRLRPHLTRCANITIIEHOKCENAYPGNITDTMVCASVOBGKXDCSGDGG	184
Db	118	GWGLLANG--RMTVLCQNVSVVSEEVCSKLYDPLYPHSMFCAGGQDQKDSNGDGG	175
Qy	185	PLVCNOSLOGIISWGQDPCAIATRKPGVYTVKCVYVDWIQETMK	227
Db	176	PLICNGYLOGLVFGKAPCGQGVGVYTNLCKFTWIEKTQV	218
RESULT 22			
US-10-294-025-327			
; Sequence 327, Application US/10294025			
; Publication No. US20030185830A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Stoik, John A.			
; APPLICANT: Kalos, Michael D.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121.427C29			
; CURRENT APPLICATION NUMBER: US/10/294,025			
; CURRENT FILING DATE: 2002-11-12			
; NUMBER OF SEQ ID NOS: 1038			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 327			
; LENGTH: 220			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-294-025-327			
Query Match 41.4%; Score 520.5; DB 14; Length 220;			
Best Local Similarity 42.2%; Pred. No. 3.4e-44;			
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3			
Qy	6	ECKPHSPQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLOHNLQ-KEEGCEQ	64
Db	2	DCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLGLHSLEADQEPGSQ	61
Qy	65	TRTATESFPHPGFNNSLPNKDRNDIMLVKASPVSIWTAVRPTLTSSRCVTAGTSCLS	124
Db	62	MVEASLSVRHPEYNRPL-----LANDMLMLIKLDESVSSEDTIRSIASQCFTAGNSCLVS	117
Qy	125	GWGSTSSPQRLRPHLTRCANITIIEHOKCENAYPGNITDTMVCASVOBGKXDCSGDGG	184
Db	118	GWGLLANG--RMTVLCQNVSVVSEEVCSKLYDPLYPHSMFCAGGQDQKDSNGDGG	175
Qy	185	PLVCNOSLOGIISWGQDPCAIATRKPGVYTVKCVYVDWIQETMK	227
Db	176	PLICNGYLOGLVFGKAPCGQGVGVYTNLCKFTWIEKTQV	218

RESULT 23
US-10-051-874-101
Sequence 101, Application US/10051874
Publication No. US2004005557A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Sytek, Kimberly A
APPLICANT: Baldog, Perenc AM
APPLICANT: Varnes, Corine AM
APPLICANT: Lu, Li
APPLICANT: Shenoy, Suresh G
APPLICANT: Casman, Stacie J
APPLICANT: Guo, Xiaojia Sasha
APPLICANT: Edinger, Shlomit R
APPLICANT: MacDougall, John R
APPLICANT: Malyankar, Uriel M
APPLICANT: Patturajan, Meesa
APPLICANT: Shimkets, Richard A

APPLICANT: Pena, Carol EA
APPLICANT: Tchernev, Velizar T
APPLICANT: Zerhusen, Bryan D
APPLICANT: Millet, Isabelle
APPLICANT: Miller, Charles E
APPLICANT: Lepley, Denise M
APPLICANT: Smithson, Glenda
APPLICANT: Baumgartner, Jason C
APPLICANT: Herrman, John L
APPLICANT: Peyman, John A
APPLICANT: Gorman, Linda
APPLICANT: Mezes, Peter D
APPLICANT: Kekuda, Ramesh
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Gerlach, Valerie
APPLICANT: Grosse, William M
APPLICANT: Liu, Xiaohong
APPLICANT: Ellerman, Karen
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Burgess, Catherine E
TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/325,306
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/272,409
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/291,672
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/330,336
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/265,530
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/261,376
PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 101
LENGTH: 229
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Tryp Spc,
OTHER INFORMATION: Trypsin-like serine protease domain sequence
US-10-051-874-101

Query Match 40.3%; Score 507.5; DB 15; Length 229;
Best Local Similarity 47.4%; Pred. No. 7.4e-43;
Matches 111; Conservative 30; Mismatches 76; Indels 17; Gaps 8;

QY 1 IIKGFECKPHSQPQWQAALFEK--TRLLCGATLIAPRWLLTAHCL---KPRYIVHLGQHN 55
DB 1 IVGSEANIGSFPMQVSLQYRGGRHFCGSLISPRWVLTAAHCYVGSAPSSIRVRLGSHD 60
QY 56 LQKEGCEQRTTATESPPHGFNNSLPNKDHRNDIMLVKMASPVSIWAVRPLTL--SSR 113
DB 61 LSSGEE--TQTVKSKVIVHPNYNPS-----TYDNDIALLLKLEPVTLSDTVRPCLPSSGY 115
QY 114 CVTAGTCLISGWSGTSPPQLRPHLTRCANITIEHOKCENAYPGN--ITDITMVCASVQ 171
DB 116 NVPAGTCTVSGWGTSESSGSLPDTLQEVNPIVSNATCRRAYSGPAITDNLGAGGL 175

QY 172 EGGKDCQDGGSGPLVCNQSG---LQGIISWGQDPCAITRKPGVYTVKVKYVDWI 222
DB 176 EGGKDACQDGGSGPLVCNDPRWLVGIVSGSYCCARPNGVYTVRVSSYLDWI 229

RESULT 24
US-09-825-751A-72
Sequence 72, Application US/09825751A
Publication No. US20030065140A1
GENERAL INFORMATION:
APPLICANT: Curagen Corporation
APPLICANT: Vernet, Corine A.M.
APPLICANT: Fernandes, Elma R.
APPLICANT: Taupier, Raymond J
APPLICANT: Quinn, Kerry E
APPLICANT: Spyttek, Kimberly A
APPLICANT: Rastelli, Luca
APPLICANT: Herrman, John L
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-750
CURRENT APPLICATION NUMBER: US/09/825,751A
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/194,314
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 60/225,693
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 72
LENGTH: 229
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: Sequence
US-09-825-751A-72

Query Match 40.3%; Score 507; DB 12; Length 229;
Best Local Similarity 47.2%; Pred. No. 8.3e-43;
Matches 110; Conservative 30; Mismatches 77; Indels 16; Gaps 7;

QY 1 IIKGFECKPHSQPQWQAALFEK--TRLLCGATLIAPRWLLTAHCL---KPRYIVHLGQHN 55
DB 2 IVGSEANIGSFPMQVSLQYRGGRHFCGSLISPRWVLTAAHCYVGSAPSSIRVRLGSHD 61
QY 56 LQKEGCEQRTTATESPPHGFNNSLPNKDHRNDIMLVKMASPVSIWAVRPLTL--SSR 113
DB 62 LSSGEE--TQTVKSKVIVHPNYNPS-----TYDNDIALLLKLEPVTLSDTVRPCLPSSGY 116
QY 114 CVTAGTCLISGWSGTSPPQLRPHLTRCANITIEHOKCENAYPGN--ITDITMVCASVQ 172
DB 117 NVPAGTCTVSGWGTSESSGSLPDTLQEVNPIVSNATCRRAYSGPAITDNLGAGGLE 176
QY 173 GKGKDCQDGGSGPLVCNQSG---LQGIISWGQDPCAITRKPGVYTVKVKYVDWI 222
DB 177 GKGKDACQDGGSGPLVCNDPRWLVGIVSGSYCCARPNGVYTVRVSSYLDWI 229

RESULT 25
US-10-071-214-49
Sequence 49, Application US/10071214
Publication No. US20030066099A1
GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: EGERUD, Torbjorn
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
FILE REFERENCE: HANSSON-3A
CURRENT APPLICATION NUMBER: US/10/071,214
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,422
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: DK PA 2001 00218
PRIOR FILING DATE: 2001-02-09

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Trypsin
; OTHER INFORMATION: Consensus Sequence
US-09-981-151A-97

Query Match 37.4%; Score 470.5; DB 11; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

QY 1 IIKGFECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58
| :
Db 1 IVGREAQAGSPFQVSLQVSSGHFCGGLISENWLTAACHCVSGASSVRVVLGEHNLGT 60
| :
QY 59 EBGCEQTRATSFPHGPFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTI--SSRCVT 116
| :
Db 61 TGTGTEQKDFVKLIIVHPNYN-----PTNDIALKLKSPVLGDTVRPICLSASSDLP 114
| :
QY 117 AGTSLISGWSTSPQLRPHLTRCANITIIHQKCNAYPGNITDTMVCASVQEGGKD 176
| :
Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVSVRETCSRAYSAGGTGTTDMICAGAL-GGKD 171
| :
QY 177 SCQDGGGLVLCNQ-SLQGIISWGQDPCATRKGVYTKVCKYVDWI 222
| :
Db 172 ACQDGGGLVLCSDGELGVISWGYG-CAVGNYPGVYTRVSRYLDMI 217
| :

RESULT 30
US-10-042-865-156
; Sequence 156, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Salomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik

; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-156

Query Match 37.4%; Score 470.5; DB 12; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

QY 1 IIKGFECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58
| :
Db 1 IVGREAQAGSPFQVSLQVSSGHFCGGLISENWLTAACHCVSGASSVRVVLGEHNLGT 60
| :
QY 59 EBGCEQTRATSFPHGPFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTI--SSRCVT 116
| :
Db 61 TGTGTEQKDFVKLIIVHPNYN-----PTNDIALKLKSPVLGDTVRPICLSASSDLP 114
| :
QY 117 AGTSLISGWSTSPQLRPHLTRCANITIIHQKCNAYPGNITDTMVCASVQEGGKD 176
| :
Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVSVRETCSRAYSAGGTGTTDMICAGAL-GGKD 171
| :
QY 177 SCQDGGGLVLCNQ-SLQGIISWGQDPCATRKGVYTKVCKYVDWI 222
| :
Db 172 ACQDGGGLVLCSDGELGVISWGYG-CAVGNYPGVYTRVSRYLDMI 217
| :

RESULT 31
US-10-072-012-805
; Sequence 805, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-258

; CURRENT APPLICATION NUMBER: US/10/072,012

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: 60/265,102

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/265,514

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,517

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,412

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,395

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/266,406

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/266,767

; PRIOR FILING DATE: 2001-02-05

; PRIOR APPLICATION NUMBER: 60/267,057

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/266,975

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/267,459

; PRIOR FILING DATE: 2001-02-08

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1391

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 805

; LENGTH: 217

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Trypsin

; OTHER INFORMATION: Consensus Sequence

US-10-072-012-805

Query Match 37.4%; Score 470.5; DB 12; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

Qy 1 IIGFECKPHSQPQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58

Db 1 IVGREGAAGSFPQVSLQVSSGHFCGSLISENNWLTAAHCVSGASSVRVVLGEHNLGT 60

Qy 59 EBGCEQRTATSPFHPGPNNSLPNKDHRNDIMLVKMASPVSIWAVRPLTL--SSRCVT 116

Db 61 TEGTEQKFDVKKIIVHPNYN-----PDTNDIALLLKSPVTLGDTVRPCLPSASSDLP 114

Qy 117 AGTSCLSISGWGSTSSPOLRPLPHTLRCAITIIIEHCKENAYPGNITDTWVCASVQEGGKD 176

Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVIVRETCRSAYGGTVDTMICAGAL--GGKD 171

Qy 177 SCQDSGGPLVCNQ--SLOGIISWGQDPCATRKPGVTVKCKYVDWI 222

Db 172 ACQDSGGPLVCSDBGELVGVSWGYG--CAVGNPGVTVTRVSRYLDWI 217

RESULT 32

US-10-072-012-813

; Sequence 813, Application US/10072012

; Publication No. US2004003493A1

; GENERAL INFORMATION:

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberly

; APPLICANT: Zerkusen, Bryan

; APPLICANT: Patturajan, Meera

; APPLICANT: Shimkets, Richard

; APPLICANT: Li, Li

; APPLICANT: Gangolli, Esha

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Anderson, David W.

; APPLICANT: Rastelli, Luca

; APPLICANT: Miller, Charles E.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Taupier Jr, Raymond J.

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Colman, Steven D.

; APPLICANT: Wolenc, Adam R.

; APPLICANT: Pena, Carol B. A.

; APPLICANT: Furtak, Katarzyna

; APPLICANT: Grosse, William M.

; APPLICANT: Alsobrook II, John P.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-258

; CURRENT APPLICATION NUMBER: US/10/072,012

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: 60/265,102

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/265,514

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,517

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,412

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,395

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/266,406

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/266,767

; PRIOR FILING DATE: 2001-02-05

; PRIOR APPLICATION NUMBER: 60/267,057

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/266,975

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/267,459

; PRIOR FILING DATE: 2001-02-08

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1391

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 813

; LENGTH: 217

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Trypsin

; OTHER INFORMATION: Consensus Sequence

US-10-072-012-813

Query Match 37.4%; Score 470.5; DB 12; Length 217;

Best Local Similarity 44.1%; Pred. No. 3.8e-39;

Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

Qy 1 IIGFECKPHSQPQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58

Db 1 IVGREGAAGSFPQVSLQVSSGHFCGSLISENNWLTAAHCVSGASSVRVVLGEHNLGT 60

Qy 59 EBGCEQRTATSPFHPGPNNSLPNKDHRNDIMLVKMASPVSIWAVRPLTL--SSRCVT 116

Db 61 TEGTEQKFDVKKIIVHPNYN-----PDTNDIALLLKSPVTLGDTVRPCLPSASSDLP 114

Qy 117 AGTSCLSISGWGSTSSPOLRPLPHTLRCAITIIIEHCKENAYPGNITDTWVCASVQEGGKD 176

Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVIVRETCRSAYGGTVDTMICAGAL--GGKD 171

Qy 177 SCQDSGGPLVCNQ--SLOGIISWGQDPCATRKPGVTVKCKYVDWI 222

Db 172 ACQDSGGPLVCSDBGELVGVSWGYG--CAVGNPGVTVTRVSRYLDWI 217

RESULT 33

US-10-037-417-136

; Sequence 136, Application US/10037417

; Publication No. US20040052806A1

OTHER INFORMATION: Description of Artificial Sequence: Trypsin
US-10-032-189-67

Query Match 37.4%; Score 470.5; DB 14; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;
QY 1 IIKGFECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58
Db 1 IVGREQAQGFQWQVLSQVSSGHFCGSLISNNWVLTAAHCVGASSVRVLGEHNLGT 60
QY 59 BEGCEQTRTATESPPHGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTL--SSRCVT 116
Db 61 TEGTEQKFDVKKIIVHNNY-----PDTNDIALLLKSPVTLGDTVRPICLPSASSDLP 114
QY 117 AGTSCLSLGGWSTSSPOLRLPHILRCANITIIHOKENAYPGNITDTMVCASVQEGGKD 176
Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVIVSRCTCRSAYGTVTDTMTCAGAL--GGKD 171
QY 177 SCQDSSGGLVPCNQ-SLQGIISWGQDPFCATRKPGVYTKVKYVDWI 222
Db 172 ACQDSSGGLVPCSDGELGVISWGYG-CAVGNYPGVYTVRSRYLDWI 217

RESULT 35

US-10-074-978A-223
Sequence 223, Application US/10074978A
Publication No. US20040010119A1

GENERAL INFORMATION:

APPLICANT: Leite, Mazio
APPLICANT: Spytek, Kimberly A
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Fernandes, Elma

APPLICANT: Li, Li
APPLICANT: Kekuda, Ramesh

APPLICANT: Liu, Xiaohong
APPLICANT: Casman, Stacie

APPLICANT: Boldog, Ferenc
APPLICANT: Patturajan, Meera

APPLICANT: Blalock, Angela
APPLICANT: Ballinger, Robert

APPLICANT: Vernet, Corine
APPLICANT: Tchernev, Velizar T

APPLICANT: Malyankar, Uriel M
APPLICANT: Gusev, Vladimir

APPLICANT: Rastelli, Luca
APPLICANT: Mezes, Peter S

APPLICANT: Ellerman, Karen
APPLICANT: Heyes, Melvin P

APPLICANT: Herrman, John
APPLICANT: Pena, Carol E A

APPLICANT: Shinkets, Richard A
APPLICANT: Taupier Jr, Raymond J

APPLICANT: Moore, No. US20040010119A1
APPLICANT: Shenoy, Suresh

APPLICANT: Edinger, Shlomit
APPLICANT: Gunther, Erik

APPLICANT: Stone, Dave
APPLICANT: Millet, Isabelle

APPLICANT: Peyman, John
APPLICANT: Smithson, Glenda

FILE REFERENCE: 21402-269
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

CURRENT APPLICATION NUMBER: US/10/074,978A
CURRENT FILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: 60/268,221
PRIOR FILING DATE: 2001-02-12

PRIOR APPLICATION NUMBER: 60/335,109
PRIOR FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: 60/312,284
PRIOR FILING DATE: 2001-08-14

PRIOR APPLICATION NUMBER: 60/268,496

PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/276,703
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/330,293
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/322,127
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/280,899
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/310,797
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/268,646
PRIOR FILING DATE: 2001-02-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 547
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 223
LENGTH: 217
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Trypsin-like
OTHER INFORMATION: serine protease domain sequence
US-10-074-978A-223

Query Match 37.4%; Score 470.5; DB 15; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

QY 1 IIKGFECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58
Db 1 IVGREQAQGFQWQVLSQVSSGHFCGSLISNNWVLTAAHCVGASSVRVLGEHNLGT 60
QY 59 BEGCEQTRTATESPPHGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTL--SSRCVT 116
Db 61 TEGTEQKFDVKKIIVHNNY-----PDTNDIALLLKSPVTLGDTVRPICLPSASSDLP 114
QY 117 AGTSCLSLGGWSTSSPOLRLPHILRCANITIIHOKENAYPGNITDTMVCASVQEGGKD 176
Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVIVSRCTCRSAYGTVTDTMTCAGAL--GGKD 171
QY 177 SCQDSSGGLVPCNQ-SLQGIISWGQDPFCATRKPGVYTKVKYVDWI 222
Db 172 ACQDSSGGLVPCSDGELGVISWGYG-CAVGNYPGVYTVRSRYLDWI 217

RESULT 36

US-10-055-569A-97

Sequence 97, Application US/10055569A
Publication No. US20040024181A1

GENERAL INFORMATION:

APPLICANT: Gangolli, Esha A

APPLICANT: Spytek, Kimberly A

APPLICANT: Gilbert, Jennifer

APPLICANT: Casman, Stacie

APPLICANT: Blalock, Angela

APPLICANT: Li, Li

APPLICANT: Vernet, Corine

APPLICANT: Shenoy, Suresh

APPLICANT: Mishra, Vishnu S

APPLICANT: Furtak, Katarzyna

APPLICANT: Gerlach, Valerie L

APPLICANT: Edinger, Shlomit

APPLICANT: Malyankar, Uriel

APPLICANT: Stone, David

APPLICANT: Millet, Isabelle

APPLICANT: Smithson, Glenda

APPLICANT: Gunther, Erik

APPLICANT: Ellerman, Karen

APPLICANT: Padigaru, Muralidhara

APPLICANT: Taupier Jr., Raymond J

APPLICANT: Anderson, David W

TITLE OF INVENTION: No. US20040024181A1e1 Human Proteins, Polynucleotides Encoding The

```
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 21402-191
; CURRENT APPLICATION NUMBER: US/10/055,569A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/243,642
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,320
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,592
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,681
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/243,863
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/244,443
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 60/245,029
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/244,995
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/245,293
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/245,315
; PRIOR FILING DATE: 2000-11-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-569A-97
```

```
Query Match 37.4%; Score 470.5; DB 16; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

Qy 1 IIKGFCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LQGHNLQK 58
Db 1 IVGREAQAGFPQVSLQVSSGHFCGSLISENWLTAHCVSGASSVRVVLGEHNLGT 60

Qy 59 EGCQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPVISITWAVRPLT--SSRCVT 116
Db 61 TEGTEQKFEVKKIIVHPNYN-----PDTNIALKLKSPVTLGDTVRPICLPSSADLP 114

Qy 117 AGTSLISGWSTSPQLRPLHPTLRCANITIEHOKCENAYPGNITDTMVCASVQEGGKD 176
Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVPIVSRCTCSAYGCTVDTMI CAGAL--GGKD 171

Qy 177 SCQDSGGPLVCNQ-SLOGIISWGDQPCATRKPGVYTKVKYVDWI 222
Db 172 ACQDSGGPLVCSDGELVGSWGYG-CAVGNYPGVYTRVSRYLDMI 217
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```
RESULT 37
US-10-262-511-104
; Publication 104, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Feyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
```

```
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 104
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-104

Query Match 37.2%; Score 468; DB 12; Length 224;
Best Local Similarity 42.3%; Pred. No. 7e-39;
Matches 87; Conservative 33; Mismatches 77; Indels 6; Gaps 2;

Qy 1 IIKGFCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLQKEE 60
Db 16 IIDGAPCARGSHPWQVALLSGNQLHCGGVLVNERWVLTAAHCKXNNEVTVHLGSDTLGDRR 75

Qy 61 GCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPVISITWAVRPLTLSSSCVTAGTS 120
Db 76 A--QRKASKSFRHPGYS---TQTHVNDLMLVKLNSQARLSSMWKVRLPSPCEPFGTT 129

Qy 121 CLISGWSTSPQLRPLHPTLRCANITIEHOKCENAYPGNITDTMVCASVQEGGKDCSQG 180
Db 130 CTVSGWGTITSPDVTTFPSDLMLCVDVKLISPQDCTKYKQDLENSMLCAGIPDSKKNACNG 189

Qy 181 DSGGPLVCNOSLQGIISWGDQPC 203
Db 190 DSGGPLVCRGTQLQLVSWGTFFC 212

RESULT 38
US-10-051-874-102
; Sequence 102, Application US/10051874
; Publication No. US20040005557A1
```

GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Alsobrook II, John P
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Boldog, Ferenc
; APPLICANT: Vernet, Corine AM
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Casman, Stacie J
; APPLICANT: Guo, Xiaojia Sashia
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard A
; APPLICANT: Pena, Carol EA
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Miller, Isabelle
; APPLICANT: Lepley, Denise M
; APPLICANT: Smithson, Glennda
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Herrman, John L
; APPLICANT: Peyman, John A
; APPLICANT: Gorman, Linda
; APPLICANT: Mezes, Peter D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William M
; APPLICANT: Liu, Xiaohong
; APPLICANT: Ellerman, Karen
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; FILE REFERENCE: 21402-245
; CURRENT APPLICATION NUMBER: US/10/051,874
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2001-02-14
; PRIOR FILING DATE: 2001-09-27
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-05-17
; PRIOR FILING DATE: 2001-10-18
; PRIOR FILING DATE: 2001-01-31
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Trypsin domain
; OTHER INFORMATION: sequence
US-10-051-874-102

Query Match 37.0%; Score 465.5; DB 15; Length 215;
Best Local Similarity 44.2%; Pred. No. 1.2e-38;
Matches 99; Conservative 34; Mismatches 76; Indels 15; Gaps 7;
QY 4 GFECKPHSQWQAALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVH--LGOHNLQKEEG 61
DB 2 GREAQAGFPQVSLQVSSGHFCGSLISENWVLTAAHCVSGASSVRVLTGEHNLGTTEG 61
QY 62 CEQRTATSPPHGPFNNSLPNKDHNDIMLVKMASPVSTWAVRPLTL--SSRCVVTAGT 119
DB 62 TEQKFDVKKIIVHFNYN-----PDTNDIALLLKLSPTLTGDTVRPICLFSASSDLPGVT 115
QY 120 SCLISGHWSTSSPOLRLPHILRCANIYIIHOKENAYPGNITDTWVCASVQGGKDSQ 179
DB 116 TCSVSGWGRTKN--LGTSDTLQEVVVPVIVSRCTCRSAYGTVTDTMTCAGAL--GGKDACQ 172
QY 180 GDSGGPLVCNQ--SLQGIISWGQDPCAITRKPVGVTYKVKYVDWI 222
DB 173 GDSGGPLVCSGDELGVISWGYG-CAVGNYPGVYTVRSRYLDWI 215
RESULT 39
US-10-325-745-4
; Sequence 4, Application US/10325745
; Publication No. US20030135028A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
; FILE REFERENCE: PF391D1
; CURRENT APPLICATION NUMBER: US/10/325,745
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 09/244,111
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 60/073,961
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-325-745-4
Query Match 36.8%; Score 463; DB 14; Length 207;
Best Local Similarity 44.6%; Pred. No. 2e-38;
Matches 87; Conservative 34; Mismatches 70; Indels 4; Gaps 3;
QY 32 APRW--LLTAHCLKPRYIVHLCQHNLOKEEGCEQTRTATESPHFGFNNSLPNKDHND 89
DB 9 AKTMMFLLLGGAWAGKYTVRLGDHSLQNKDGEQEPVQVQSIHPHCYNSS--DVEDHND 67
QY 90 IMLVMAASPVSTWAVRPLTLSSRCVVTAGTSCLSGWSSTSSPOLRLPHILRCANITIE 149
DB 68 LMLQLRDQASLGSVKYKPSLADHCTQLAESAFSQAGGVTSRENFPTDNLCAEVKSP 127
QY 150 HKCENAYPGNITDTWVCASVQGGKDSQCGDSGGPLVNCQSLQGIISWGQDPCAITRKP 209
DB 128 QKKCEDAYPGQITDGMVYAGSSXGA-DTCQDSSGGLVCDGALQGITSWGSDPCGRSDXP 186
QY 210 GVTYKVKYVDWIQ 224
DB 187 GVTNCRILDWIKK 201
RESULT 40
US-10-004-378A-147
; Sequence 147, Application US/10004378A
; Publication No. US20030228301A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Furtak, Kazaryna
; APPLICANT: Perna, Amanda
; APPLICANT: Patturajan, Meera

APPLICANT: Shimkets, Richard A
APPLICANT: Guo, Xiaojia Sasha
APPLICANT: Casman, Stacie J
APPLICANT: Burgess, Catherine E
APPLICANT: Malyankar, Uriel M
APPLICANT: Tchernev, Vellizar T
APPLICANT: Vernet, Corrine A
APPLICANT: Spytek, Kimberly A
APPLICANT: Ages, Michele
APPLICANT: Rastelli, Luca
APPLICANT: Shenoy, Suresh G
APPLICANT: Grosse, William M
APPLICANT: Alsbrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Gerlach, Valerie
APPLICANT: Edinger, Schlomit
APPLICANT: MacDougall, John R
APPLICANT: Feyman, John A
APPLICANT: Gunther, Erik
APPLICANT: Stone, David J
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha A
TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding TH
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 21402-179
CURRENT APPLICATION NUMBER: US/10/004,378A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/242,882
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,765
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/300,206
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/242,789
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,768
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,767
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/243,622
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/273,047
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/243,591
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,950
PRIOR FILING DATE: 2000-10-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 147
LENGTH: 207
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Trypsin domain
US-10-004-378A-147

Query Match 36.5%; Score 459.5; DB 15; Length 207;
Best Local Similarity 44.7%; Pred. NO. 4.6e-38;
Matches 97; Conservative 33; Mismatches 72; Indels 15; Gaps 7;

QY 11 SOPWQALPEKTELLCGATLIAPRWLLTAACLKPRYIVH--LGOHNLQKEGCEQTRTA 68
Db 1 SPFWQVSLQVSGHFGCGSLIENWVLTAAHCVSASSVRVVLGHNLTGTEGQKFDV 60
QY 69 TESFPHEFGNNSLPNKHNDIMLVKMASFVSITWAVREPLT--SSRCVTAAGTSLISGW 126
Db 61 KXIIVHPNPN-----PDNDIALLLKSPVTLGDTVRPCLPSSASDLPGVTTCSVSGW 114
QY 127 GSTSSPQLRLPHTLRANTITIEHQENAYFQGNITDTWCVASVQEGKDSQCGSGGPL 186

Db 115 GRTKN--LGTSDTLQEVVPIVSRETCSRSAVGTVDTMTICAGAL-GGKDACQDSGGPL 171
QY 187 VCNQ-SLOGIISWGQDPFCATRKPGVYTKYKVDWI 222
Db 172 VCSDELGVISWGYG-CAVGNTPGVTVRSRYLDWI 207

RESULT 41
US-10-036-371-8
Sequence 8, Application US/10036371
Publication No. US20020141987A1
GENERAL INFORMATION:
APPLICANT: BJARNARSON, JON B.
TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND
TITLE OF INVENTION: COSMETIC USE
FILE REFERENCE: 81691/284960
CURRENT APPLICATION NUMBER: US/10/036,371
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 09/411,688
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 5086/99
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 225
TYPE: PRT
ORGANISM: Gadus sp.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (9)
OTHER INFORMATION: K or R
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (24)
OTHER INFORMATION: Y or F
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (32)
OTHER INFORMATION: K or E
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (33)
OTHER INFORMATION: D or Q
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (64)
OTHER INFORMATION: Y or F
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (71)
OTHER INFORMATION: I or unknown
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (82)
OTHER INFORMATION: N or D
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (92)
OTHER INFORMATION: K or E
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (123)
OTHER INFORMATION: A or D
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (136)
OTHER INFORMATION: V or C
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (138)
OTHER INFORMATION: N or S
FEATURE:

; NAME/KEY: MOD_RES
; LOCATION: (204)
; OTHER INFORMATION: H or N
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (212)
; OTHER INFORMATION: M, V or C
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (224)
; OTHER INFORMATION: N or S
US-10-036-371-8

Query Match 35.9%; Score 451; DB 13; Length 225;
Best Local Similarity 41.0%; Pred. No. 3.7e-37;
Matches 94; Conservative 38; Mismatches 87; Indels 10; Gaps 6;

Qy 1 IIGFECKPHSOPQAALEFETRLLCGATLIAPRWLLTAHCLKPRYIVHLGOHNLQKEE 60
Db 1 IVGFECKPHSOPQAALEFETRLLCGATLIAPRWLLTAHCLKPRYIVHLGOHNLQKEE 60
Qy 61 GCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTTAGTS 120
Db 60 GTEQXISSSVSRHPNYS---SYNIXNDIMLIKLPATLNGYVHAVALPTECAADATM 115
Qy 121 CLISGWGSTSPQRLPHTLRNCANITIEHQKENAY-PGNIITDTWVCASVQBGKDSQ 179
Db 116 CTVSGWNTWS-SYXGDGKLXLPLSHADCANSGPGMITQSMFCAGYLEGGKDSQ 174
Qy 180 GDSGGLVNCQSLQ--GIISWGDPCAITRKPGYTKVCKYVDWIOETM 226
Db 175 GDSGPPVGVNLQGVGVSWGYG-CAERXPVGYYAKYXVLSGWVDTM 222

RESULT 42
US-09-759-143-176
; Sequence 176, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(205)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-759-143-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

Qy 21 KTRLLCGATLIAPRWLLTAHCLKPRYIVHLGOHNLQ-KEEGCEQTRTATESPFPFGFNN 79
Db 2 ENELFCGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQEPGQMVYASLSVRHPEYNR 61
Qy 80 SLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTTAGTSCLISGWGSTSPQRLPHT 139
Db 62 LL----LANDMLIKLDESSESITIRISIASOCPAGNSCLVSGHGLANG--RNPTV 115
Qy 140 LRCANITIEHQKENAYPGNIITDTWVCASVQBGKDSQCGDGLVNCQSLQGIISWG 199
Db 116 LHCNVSVVSVXVCKLYDPLYPHSMFCAGGQDQKSCNGDGGPLICNGYLQGLVSGF 175
Qy 200 QDPCAITRKPGYTKVCKYVDWIOETMK 227
Db 176 KAPCQLGVPGVYTNLUCKFTWIEKTVQ 203

RESULT 43
US-09-780-669-176
; Sequence 176, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(205)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-780-669-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

Qy 21 KTRLLCGATLIAPRWLLTAHCLKPRYIVHLGOHNLQ-KEEGCEQTRTATESPFPFGFNN 79
Db 2 ENELFCGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQEPGQMVYASLSVRHPEYNR 61
Qy 80 SLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTTAGTSCLISGWGSTSPQRLPHT 139

Db 62 LL-----LANDMLIKLDESSESDTIRSIASQCTAGNSCLVSGWGLLANG--RMPTV 115

QY 140 LRCANITIIHQKCNAYPGNITDTMVCASVQEGKDCQGDGGPLVNCNOSLOGIISWG 199

Db 116 LHCNVSVVSEKXVCKLYDPLYPHPSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSFG 175

QY 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227

Db 176 KAPCQQLGVPGVYTNLCKFTWIEKTVQ 203

RESULT 44

US-09-030-606-176

Sequence 176, Application US/09030606

Patent No. US20020081580A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS

NUMBER OF SEQUENCES: 224

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,606

FILING DATE: 25-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.428C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 176:

SEQUENCE CHARACTERISTICS:

LENGTH: 205 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-09-030-606-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;

Best Local Similarity 39.9%; Pred. No. 7.4e-37;

Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

QY 21 KTRLGCGATLIAPRWLLTAHCLKPRYIVHLGQHNLQ-KEEGCEQTRTATESFPHGPN 79

Db 2 ENELFCSGVLVHPQWLSAAHCFQNSYITGLHLSLEADQEPGSMVEASLSVRHPEYNR 61

QY 80 SLPNKHNRNDIMLVKASPVSIWAVRPLTSLSRCTAGTSCILISGWSGTSPPQLRLPHT 139

Db 62 LL-----LANDMLIKLDESSESDTIRSIASQCTAGNSCLVSGWGLLANG--RMPTV 115

QY 140 LRCANITIIHQKCNAYPGNITDTMVCASVQEGKDCQGDGGPLVNCNOSLOGIISWG 199

Db 116 LHCNVSVVSEKXVCKLYDPLYPHPSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSFG 175

QY 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227

Db 176 KAPCQQLGVPGVYTNLCKFTWIEKTVQ 203

RESULT 46

US-09-115-453-176

Sequence 176, Application US/09115453B

Patent No. US20020090372A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

FILE REFERENCE: 210121.427C4

CURRENT APPLICATION NUMBER: US/09/115,453B

CURRENT FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 176

LENGTH: 205

TYPE: PRT

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(205)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-115-453-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;

Best Local Similarity 39.9%; Pred. No. 7.4e-37;

Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

RESULT 45

US-09-822-827-176

Sequence 176, Application US/09822827

Patent No. US20020081680A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 176

LENGTH: 205

TYPE: PRT

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(205)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-822-827-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;

Best Local Similarity 39.9%; Pred. No. 7.4e-37;

Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

QY 21 KTRLGCGATLIAPRWLLTAHCLKPRYIVHLGQHNLQ-KEEGCEQTRTATESFPHGPN 79

Db 2 ENELFCSGVLVHPQWLSAAHCFQNSYITGLHLSLEADQEPGSMVEASLSVRHPEYNR 61

QY 80 SLPNKHNRNDIMLVKASPVSIWAVRPLTSLSRCTAGTSCILISGWSGTSPPQLRLPHT 139

Db 62 LL-----LANDMLIKLDESSESDTIRSIASQCTAGNSCLVSGWGLLANG--RMPTV 115

QY 140 LRCANITIIHQKCNAYPGNITDTMVCASVQEGKDCQGDGGPLVNCNOSLOGIISWG 199

Db 116 LHCNVSVVSEKXVCKLYDPLYPHPSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSFG 175

QY 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227

Db 176 KAPCQQLGVPGVYTNLCKFTWIEKTVQ 203

RESULT 46

US-09-115-453-176

Sequence 176, Application US/09115453B

Patent No. US20020090372A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

FILE REFERENCE: 210121.427C4

CURRENT APPLICATION NUMBER: US/09/115,453B

CURRENT FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 176

LENGTH: 205

TYPE: PRT

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(205)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-115-453-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;

Best Local Similarity 39.9%; Pred. No. 7.4e-37;

Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

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Qy 21 KTRLLCGATLIAPRWLLTAHCLKPRYIVHLGOHNLQ-KEEGCEQTRTATESPPHGFNN 79
Db 2 ENELFCGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSQMVSEASLSVRHPEYNR 61
Qy 80 SLPNKDRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCLSGWSGTSSPQLRLPHT 139
Db 62 LL-----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWGLLANG--RMPVT 115
Qy 140 LRCANITIIHOKCENAYPGNITDTWVCASVQEGGKDSGCGSGGPLVNCOSLQGIISWG 199
Db 116 LHCNVSVSVSEKSLYDPLVHPSMFCAGGGQDKDSCNGDSGGPLICNGVLQGLVSFG 175
Qy 200 QDPCAITRKPGVYTKVCKYVDWTQETMK 227
Db 176 KAPCGQLGVPGVYTNLCKFTWIEKTVQ 203

```

RESULT 47

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US-09-232-880-176
; Sequence 176, Application US/09232880
; Publication No. US20020192596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232.880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(205)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-232-880-176

```

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Query Match 35.6%; Score 447.5; DB 9; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

Qy 21 KTRLLCGATLIAPRWLLTAHCLKPRYIVHLGOHNLQ-KEEGCEQTRTATESPPHGFNN 79
Db 2 ENELFCGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSQMVSEASLSVRHPEYNR 61
Qy 80 SLPNKDRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCLSGWSGTSSPQLRLPHT 139
Db 62 LL-----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWGLLANG--RMPVT 115
Qy 140 LRCANITIIHOKCENAYPGNITDTWVCASVQEGGKDSGCGSGGPLVNCOSLQGIISWG 199
Db 116 LHCNVSVSVSEKSLYDPLVHPSMFCAGGGQDKDSCNGDSGGPLICNGVLQGLVSFG 175
Qy 200 QDPCAITRKPGVYTKVCKYVDWTQETMK 227
Db 176 KAPCGQLGVPGVYTNLCKFTWIEKTVQ 203

```

RESULT 48

```

US-09-895-793-176
; Sequence 176, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.

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; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895.793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(205)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-793-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

Qy 21 KTRLLCGATLIAPRWLLTAHCLKPRYIVHLGOHNLQ-KEEGCEQTRTATESPPHGFNN 79
Db 2 ENELFCGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSQMVSEASLSVRHPEYNR 61
Qy 80 SLPNKDRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCLSGWSGTSSPQLRLPHT 139
Db 62 LL-----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWGLLANG--RMPVT 115
Qy 140 LRCANITIIHOKCENAYPGNITDTWVCASVQEGGKDSGCGSGGPLVNCOSLQGIISWG 199
Db 116 LHCNVSVSVSEKSLYDPLVHPSMFCAGGGQDKDSCNGDSGGPLICNGVLQGLVSFG 175
Qy 200 QDPCAITRKPGVYTKVCKYVDWTQETMK 227
Db 176 KAPCGQLGVPGVYTNLCKFTWIEKTVQ 203

RESULT 49
US-09-895-814-176
; Sequence 176, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.

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; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(205)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-814-176

Query Match          35.6%; Score 447.5; DB 9; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

QY 21 KTRLCCGATLIAPRWLLTAACHLKPRYIVHLGHNLO-KEEGCEQTRTATESFPHGPN 79
Db 2 ENELFCGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEY 61
QY 80 SLPNKDRNDIMLVKMASPVSTWAVRPLTSSRCVVTAGTSCLSISGWSTSSPOLRLPHT 139
Db 62 LL----LANDMLIKLDESVSSEDTRISISIASQCTAGNSCLVSGWGLLANG--RMPTV 115
QY 140 LRCANITIIHQKCNAYPGNITDTMVCASVQEGGKDCQGDGSGPLVNCOSLOGIISWG 199
Db 116 LHCNVSVVSEKXVCKSLYDPLVHPSMFCAGGQDQDKSCNGDSGGLICNGYLOGLVSFG 175
QY 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 KAPCGQLGVPGVYTNLCKFTEWIEKTVQ 203
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RESULT 50

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US-10-012-896-176
; Sequence 176, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
```

```
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 127, 204
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-012-896-176

Query Match          35.6%; Score 447.5; DB 13; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

QY 21 KTRLCCGATLIAPRWLLTAACHLKPRYIVHLGHNLO-KEEGCEQTRTATESFPHGPN 79
Db 2 ENELFCGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEY 61
QY 80 SLPNKDRNDIMLVKMASPVSTWAVRPLTSSRCVVTAGTSCLSISGWSTSSPOLRLPHT 139
Db 62 LL----LANDMLIKLDESVSSEDTRISISIASQCTAGNSCLVSGWGLLANG--RMPTV 115
QY 140 LRCANITIIHQKCNAYPGNITDTMVCASVQEGGKDCQGDGSGPLVNCOSLOGIISWG 199
Db 116 LHCNVSVVSEKXVCKSLYDPLVHPSMFCAGGQDQDKSCNGDSGGLICNGYLOGLVSFG 175
QY 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 KAPCGQLGVPGVYTNLCKFTEWIEKTVQ 203
```

Search completed: June 25, 2004, 15:20:19
Job time : 52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2004, 23:45:26 ; Search time 456 Seconds
(without alignment)

23000.591 Million cell updates/sec

Title: US-09-856-320A-2_COPY_54_282

Perfect score: 1258

Sequence: 1 IIKGPECKPHSQPMQALFE.....GVYIKVKYVDWIQETMKNN 229

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2194776

Minimum DB seq length: 0

Maximum DB seq length: 229

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters: -DEV=xlh

-MODE=frame+p2n.model -DEV=xlh

-O=/cgn2_1/USPTO.spool/US09856320/runat_25062004_124555_1062/app_query.fasta_1.391

-DB=Published Applications NA_QFMT=fastap -SUFFX=rnpb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blowsum62

-TRANS=human40.cdi -LIST=500 -DOALIGN=200 -THR SCORE=pct -THR MAX=100

-THR MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0

-MAXLEN=229 -USR=US09856320/CGN 1.1 485 @runat_25062004_124555_1062 -NCPU=6

-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DEEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	287	22.8	158	15	US-10-029-386-23402
2	206	16.4	153	13	US-10-344-394-24
3	202.5	16.1	205	9	US-09-777-564-697
4	202.5	16.1	205	15	US-10-015-219-697
5	194	15.4	178	13	US-10-262-511-57
6	188	14.9	202	15	US-10-029-386-21469
7	171.5	13.6	181	10	US-09-814-353-15407
8	167	13.3	188	15	US-10-029-386-21559
9	164	13.0	154	13	US-10-344-394-14
10	156	12.4	138	15	US-10-029-386-23583
11	153	12.2	203	15	US-10-029-386-24458
12	149.5	11.9	203	9	US-09-960-352-11298
13	138.5	11.0	147	15	US-10-029-386-13717
14	136	10.8	137	13	US-10-344-394-20
15	136	10.8	163	9	US-09-867-701-3234
16	131.5	10.5	216	9	US-09-885-441-16
17	131.5	10.5	216	13	US-10-424-836-16
18	129.5	10.3	154	15	US-10-029-386-23119
19	128.5	10.2	216	15	US-10-029-386-23582
20	124.5	9.9	180	15	US-10-029-386-23379
21	123	9.8	178	15	US-10-275-091-6
22	123	9.8	178	16	US-10-240-460-3
23	122	9.7	173	15	US-10-029-386-21383
24	122	9.7	196	15	US-10-029-386-26364
25	119	9.5	149	15	US-10-029-386-21960
26	117	9.3	180	15	US-10-094-507-21
27	115	9.1	182	9	US-09-864-761-28804
28	114	9.1	184	15	US-10-060-036-3294
29	114	9.1	195	15	US-10-060-036-3490
30	114	9.1	214	15	US-10-060-036-3865
31	113	9.0	205	15	US-10-060-036-3854
32	112	8.9	181	15	US-10-060-036-3798
33	112	8.9	190	15	US-10-029-386-23643
34	111.5	8.9	123	15	US-10-029-386-23238
35	109	8.7	175	15	US-10-060-036-4410
36	109	8.7	218	15	US-10-060-036-3468
37	108	8.6	220	9	US-09-864-761-27190
38	108	8.6	220	9	US-09-923-779-118
39	108	8.6	220	9	US-09-923-779-119
40	108	8.6	220	9	US-09-923-779-124
41	108	8.6	220	9	US-09-923-779-125
42	108	8.6	220	9	US-09-923-779-126
43	108	8.6	220	9	US-09-923-779-127
44	107.5	8.5	176	15	US-10-029-386-14818
45	107	8.5	118	15	US-10-029-386-26680
46	107	8.5	208	9	US-09-923-779-89
47	105	8.3	156	15	US-10-060-036-3583
48	104.5	8.3	138	9	US-09-888-615-58
49	104	8.3	157	15	US-10-060-036-3369
50	103.5	8.2	189	13	US-10-424-599-75219
51	102.5	8.1	161	15	US-10-029-386-24763
52	101.5	8.1	116	9	US-09-864-761-18438
53	101	8.0	177	13	US-10-150-813-82
54	101	8.0	177	13	US-10-139-854-82
55	101	8.0	177	15	US-10-131-403-82
56	101	8.0	177	16	US-10-150-811-82
57	101	8.0	181	13	US-09-771-357-95
58	101	8.0	181	15	US-10-059-579-95
59	101	8.0	224	15	US-10-100-178-2
60	99.5	7.9	167	15	US-10-029-386-26388
61	98	7.8	211	9	US-09-923-779-16
62	97.5	7.8	177	15	US-10-029-386-27142
63	97	7.7	167	9	US-09-885-441-17
64	97	7.7	167	13	US-10-424-836-17
65	96	7.6	65	10	US-09-908-975-25850
66	96	7.6	109	15	US-10-029-386-23346
67	95	7.6	172	9	US-09-864-761-28651
68	95	7.6	172	9	US-09-864-761-28923
69	94	7.5	134	15	US-10-029-386-23262
70	92	7.3	60	10	US-09-908-975-8568
71	92	7.3	134	13	US-09-826-734-71
72	92	7.3	211	15	US-10-029-386-27166

c 73	91	7.2	90	9	US-09-759-143-120	Sequence 120, App	146	76	6.0	65	10	US-09-908-975-1272	Sequence 1272, App
c 74	91	7.2	90	9	US-09-780-669-120	Sequence 120, App	147	76	6.0	65	10	US-09-908-975-1285	Sequence 1285, App
c 75	91	7.2	90	9	US-09-806-606-120	Sequence 120, App	148	76	6.0	65	10	US-09-908-975-1285	Sequence 1285, App
c 76	91	7.2	90	9	US-09-822-827-120	Sequence 120, App	c 149	76	6.0	227	15	US-10-060-036-3555	Sequence 3555, App
c 77	91	7.2	90	9	US-09-822-827-120	Sequence 120, App	150	76	6.0	69	15	US-10-340-860A-24	Sequence 24, Appli
c 78	91	7.2	90	9	US-09-822-827-120	Sequence 120, App	c 151	76	6.0	80	16	US-10-446-065-6	Sequence 6, Appli
c 79	91	7.2	90	9	US-09-822-827-120	Sequence 120, App	c 152	76	6.0	127	10	US-09-981-936-406	Sequence 406, App
c 80	91	7.2	90	9	US-09-822-827-120	Sequence 120, App	153	76	6.0	151	15	US-10-128-966-43	Sequence 43, Appli
c 81	91	7.2	90	14	US-10-012-896-120	Sequence 120, App	154	74	5.9	61	9	US-09-909-320-282	Sequence 282, App
c 82	91	7.2	90	15	US-10-012-896-120	Sequence 120, App	155	74	5.9	61	9	US-09-909-320-282	Sequence 282, App
c 83	91	7.2	90	15	US-10-144-678A-120	Sequence 120, App	156	74	5.9	61	9	US-09-905-291A-282	Sequence 282, App
c 84	91	7.2	90	15	US-10-294-025-120	Sequence 120, App	157	74	5.9	61	9	US-09-902-853-282	Sequence 282, App
c 85	90	7.2	147	10	US-09-991-936-414	Sequence 414, App	158	74	5.9	61	9	US-09-907-824-282	Sequence 282, App
c 86	89	7.1	102	15	US-10-029-386-23378	Sequence 23378, A	159	74	5.9	61	9	US-09-907-841-282	Sequence 282, App
c 87	86.5	6.9	192	13	US-10-621-901-1300	Sequence 1300, App	160	74	5.9	61	10	US-09-904-011-282	Sequence 282, App
c 88	86	6.8	100	15	US-10-272-665-106	Sequence 106, App	161	74	5.9	61	10	US-09-906-742-282	Sequence 282, App
c 89	86	6.8	100	15	US-10-273-321-106	Sequence 106, App	162	74	5.9	61	10	US-09-906-742-282	Sequence 282, App
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370	59	4.7	43	15	US-10-020-063A-178	Sequence 178, App	443	57	4.5	189	13	US-10-283-017-1026	Sequence 1026, Ap
371	59	4.7	43	15	US-10-015-391A-178	Sequence 178, App	444	57	4.5	189	15	US-10-017-754-1026	Sequence 1026, Ap
372	59	4.7	43	15	US-10-017-407A-178	Sequence 178, App	445	57	4.5	189	15	US-10-113-872-1026	Sequence 1026, Ap
373	59	4.7	43	15	US-10-011-833A-178	Sequence 178, App	446	57	4.5	192	9	US-09-864-761-2403	Sequence 4, Appli
374	59	4.7	43	15	US-10-006-041A-178	Sequence 178, App	447	57	4.5	200	15	US-10-109-616-4	Sequence 4, Appli
375	59	4.7	43	15	US-10-015-822A-178	Sequence 178, App	448	57	4.5	211	13	US-10-424-599-127576	Sequence 127576,
376	59	4.7	43	15	US-10-015-387A-178	Sequence 178, App	449	57	4.5	219	15	US-10-072-602B-43	Sequence 43, Appl
377	59	4.7	43	15	US-10-006-130A-178	Sequence 178, App	450	57	4.5	219	15	US-10-072-602B-46	Sequence 46, Appl
378	59	4.7	43	15	US-10-006-172A-178	Sequence 178, App	451	57	4.5	221	13	US-10-085-783A-12438	Sequence 12438, A
379	59	4.7	43	15	US-10-017-253A-178	Sequence 178, App	452	57	4.5	221	15	US-10-043-487-184	Sequence 184, App
380	59	4.7	43	15	US-10-015-392A-178	Sequence 178, App	453	57	4.5	221	16	US-10-242-535A-12438	Sequence 12438, A
381	59	4.7	43	15	US-10-017-306A-178	Sequence 178, App	454	56	4.5	142	9	US-09-864-761-31532	Sequence 31532, A
382	59	4.7	43	15	US-10-017-867A-178	Sequence 178, App	455	56	4.5	65	10	US-09-908-975-1294	Sequence 1294, Ap
383	59	4.7	43	15	US-10-012-064A-178	Sequence 178, App	456	56	4.5	144	15	US-10-029-386-21204	Sequence 21204, A
384	59	4.7	43	15	US-10-013-909A-178	Sequence 178, App	457	56	4.5	146	9	US-09-884-761-31537	Sequence 31537, A
385	59	4.7	43	15	US-10-015-671A-178	Sequence 178, App	458	56	4.5	159	15	US-10-060-036-4009	Sequence 4009, Ap
386	59	4.7	43	15	US-10-015-610A-178	Sequence 178, App	459	56	4.5	160	9	US-09-772-134B-90	Sequence 90, Appl
387	59	4.7	43	15	US-10-012-137A-178	Sequence 178, App	460	56	4.5	173	9	US-09-864-761-29419	Sequence 29419, A
388	59	4.7	43	15	US-10-012-752A-178	Sequence 178, App	461	56	4.5	198	15	US-10-156-761-2286	Sequence 2286, Ap
389	59	4.7	43	15	US-10-012-754A-178	Sequence 178, App	462	56	4.5	200	14	US-10-013-807-3	Sequence 3, Appli
390	59	4.7	43	15	US-10-013-910A-178	Sequence 178, App	463	56	4.5	200	15	US-10-179-403-3	Sequence 3, Appli
391	59	4.7	43	15	US-10-013-911A-178	Sequence 178, App	464	56	4.5	209	13	US-10-085-783A-22929	Sequence 22929, A
392	59	4.7	43	15	US-10-013-912A-178	Sequence 178, App	465	56	4.5	209	16	US-10-242-535A-22929	Sequence 22929, A
393	59	4.7	43	15	US-10-015-653A-178	Sequence 178, App	466	55	4.4	159	9	US-09-864-761-17729	Sequence 17729, A
394	59	4.7	43	15	US-10-012-101B-178	Sequence 178, App	467	55	4.4	159	9	US-09-864-761-32766	Sequence 32766, Ap
395	59	4.7	43	15	US-10-015-480A-178	Sequence 178, App	468	55	4.4	171	13	US-10-085-783A-2552	Sequence 2552, Ap
396	59	4.7	43	15	US-10-015-715A-178	Sequence 178, App	469	55	4.4	171	16	US-10-242-535A-2552	Sequence 2552, Ap
397	59	4.7	43	15	US-10-012-237A-178	Sequence 178, App	470	55	4.4	199	9	US-09-864-761-24850	Sequence 24850, Ap
398	59	4.7	43	15	US-10-013-908A-178	Sequence 178, App	471	55	4.4	207	9	US-09-960-352-13216	Sequence 13216, A
399	59	4.7	43	15	US-10-015-388A-178	Sequence 178, App	472	55	4.4	207	9	US-09-936-634-26	Sequence 26, Appl
400	59	4.7	43	15	US-10-012-753A-178	Sequence 178, App	473	55	4.4	207	10	US-09-997-182-26	Sequence 26, Appl
401	59	4.7	43	15	US-10-015-385A-178	Sequence 178, App	474	55	4.4	221	9	US-09-997-181-26	Sequence 26, Appl
402	59	4.7	43	15	US-10-007-236A-178	Sequence 178, App	475	55	4.4	221	9	US-09-294-093B-4253	Sequence 4253, Ap
403	59	4.7	43	15	US-10-015-389A-178	Sequence 178, App	476	55	4.4	222	9	US-09-974-300-6493	Sequence 6493, Ap
404	59	4.7	43	16	US-10-015-519A-178	Sequence 178, App	477	55	4.4	229	13	US-10-085-783A-11784	Sequence 11784, A
405	59	4.7	43	16	US-10-013-915A-178	Sequence 178, App	478	55	4.4	229	16	US-10-242-535A-11784	Sequence 11784, A
406	59	4.7	43	16	US-10-015-394A-178	Sequence 178, App	479	55	4.4	51	9	US-09-759-143-793	Sequence 793, App
407	59	4.7	43	16	US-10-015-390A-178	Sequence 178, App	480	55	4.4	51	9	US-09-780-669-793	Sequence 793, App
408	59	4.7	43	16	US-10-006-746A-178	Sequence 178, App	481	55	4.4	51	9	US-09-822-827-793	Sequence 793, App
409	59	4.7	43	16	US-10-011-795A-178	Sequence 178, App	482	55	4.4	51	9	US-09-895-793-793	Sequence 793, App
410	59	4.7	43	16	US-10-012-231A-178	Sequence 178, App	483	55	4.4	51	9	US-09-895-814-793	Sequence 793, App
411	59	4.7	60	15	US-10-281-043-3	Sequence 3, Appli	484	55	4.4	51	14	US-10-012-896-793	Sequence 793, App
412	59	4.7	65	10	US-09-908-975-25900	Sequence 25900, A	485	55	4.4	51	15	US-10-144-678A-793	Sequence 793, App
413	59	4.7	192	9	US-09-815-343-681	Sequence 681, App	486	55	4.4	51	15	US-10-294-025-793	Sequence 793, App
414	59	4.7	192	9	US-09-815-343-1031	Sequence 1031, App	487	55	4.4	129	13	US-10-085-783A-21017	Sequence 21017, A
415	59	4.7	192	9	US-09-920-300A-944	Sequence 944, App	488	55	4.4	129	16	US-10-242-535A-21017	Sequence 21017, A
416	59	4.7	192	13	US-10-097-105-681	Sequence 681, App	489	55	4.4	150	10	US-09-535-459-1270	Sequence 1270, Ap
417	59	4.7	192	13	US-10-097-108-1031	Sequence 1031, App	490	55	4.4	192	9	US-09-920-300A-793	Sequence 793, App
418	59	4.7	192	14	US-10-033-528-944	Sequence 944, App	491	55	4.4	192	14	US-10-033-528-793	Sequence 793, App
419	59	4.7	192	15	US-10-099-928-944	Sequence 944, App	492	55	4.4	192	15	US-10-099-926-793	Sequence 793, App
420	59	4.7	193	13	US-10-424-599-26008	Sequence 26008, A	493	55	4.4	195	9	US-09-960-352-5905	Sequence 5905, Ap
421	59	4.7	196	9	US-09-815-343-935	Sequence 935, App	494	55	4.4	213	13	US-10-424-599-32484	Sequence 32484, A
422	59	4.7	196	13	US-10-097-105-935	Sequence 935, App	495	55	4.4	222	9	US-09-864-761-32393	Sequence 32393, A
423	59	4.7	217	15	US-10-029-386-26216	Sequence 26216, A	496	55	4.4	222	9	US-09-864-761-32393	Sequence 32393, A
424	58.5	4.7	202	13	US-10-424-599-113525	Sequence 113525	497	55	4.4	225	11	US-09-864-761-32393	Sequence 2551, Ap
425	58.5	4.7	208	13	US-10-085-783A-1085	Sequence 1085, App	498	55	4.4	193	13	US-10-424-599-72239	Sequence 72239, A
426	58.5	4.7	218	16	US-10-242-535A-1085	Sequence 1085, App	499	54.5	4.3	212	15	US-10-299-497-10	Sequence 10, Appl
427	58.5	4.7	218	16	US-10-027-632-279224	Sequence 279224,	500	54.5	4.3	218	15	US-10-029-386-23914	Sequence 23914, A
428	58.5	4.7	218	16	US-10-027-632-279224	Sequence 279224,							
429	57.5	4.6	147	13	US-10-424-599-16336	Sequence 16336, A							
430	57.5	4.6	184	15	US-10-029-386-24444	Sequence 24444, A							
431	57.5	4.6	195	13	US-10-085-783A-3679	Sequence 3679, App							
432	57.5	4.6	195	16	US-10-242-535A-3679	Sequence 3679, App							
433	57.5	4.6	198	13	US-10-424-599-57894	Sequence 57894, A							
434	57	4.5	60	10	US-09-908-975-8758	Sequence 8758, App							
435	57	4.5	65	10	US-09-908-975-1284	Sequence 1284, App							
436	57	4.5	125	13	US-10-150-813-94	Sequence 94, Appl							
437	57	4.5	125	13	US-10-139-854-94	Sequence 94, Appl							

RESULT 1

US-10-029-386-23402
; Sequence 23402, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.

ALIGNMENTS


```
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23402
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.88
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: Q9UBX7, EVALUE 8.00e-27
; OTHER INFORMATION: EST HUMAN HIT: AA436049.1, EVALUE 6.00e-82
; OTHER INFORMATION: NT HIT: g114755026, EVALUE 6.00e-84
US-10-029-386-23402

Alignment Scores:
Pred. No.: 8,73e-26 Length: 158
Score: 287.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.81% Indels: 0
DB: 15 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-23402 (1-158)
QY 179 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 198
Db 2 CAGGGTGACTCCGGGGGCCCTCTGGTCTGTACCAAGTCTCTTCAAGGCATTATCTCTGG 61
QY 199 GlnGlyAspProCysAlaIleThrArgLysProGlyValThyThrLysValCysLysTyr 218
Db 62 GGCAGGATCCGTGTGCGATCACCAGGAGCTGTGTGTACACGAAAGTCTGCAATAT 121
QY 219 ValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 122 GTGGACTGATCCAGGAGACGATGAAGAACAT 154

RESULT 2
US-10-344-394-24
; Sequence 24, Application US/10344394
; Publication No. US20040058342A1
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OF INVENTION: NOVEL KALLIKREIN GENE
; FILE REFERENCE: 11757.51USWO
; CURRENT APPLICATION NUMBER: US/10/344,394
; CURRENT FILING DATE: 2003-02-11
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/CA01/01141
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-344-394-24

Alignment Scores:
Pred. No.: 5,33e-16 Length: 153
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Score: 206.00 Matches: 36
Percent Similarity: 80.00% Conservative: 4
Best Local Similarity: 72.00% Mismatches: 10
Query Match: 16.38% Indels: 0
DB: 13 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-344-394-24 (1-153)
QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 199
Db 1 GGTGACTCTGGGGAGCCCTGTCTGTGGGGGCATCTCGAGGGCATTGTGTCTCTGGGGT 60
QY 200 GlnAspProCysAlaIleThrArgLysProGlyValThyThrLysValCysLysTyrVal 219
Db 61 GAGTCCCTTGTGACACACACCACCAAGCCCTGGTGTATACCAAGTCTGCCACTACTTG 120
QY 220 AspTrpIleGlnGluThrMetLysAsnAsn 229
Db 121 GAGTGGATCAGGGAACCATGAAGAGAAC 150

RESULT 3
US-09-777-564-697
; Sequence 697, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 21021.493
; CURRENT APPLICATION NUMBER: US/09/777,564
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SOFTWARE: FastSeq for Window Version 4.0
; SEQ ID NO 697
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-564-697

Alignment Scores:
Pred. No.: 2,12e-15 Length: 205
Score: 202.50 Matches: 34
Percent Similarity: 73.53% Conservative: 16
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 16.10% Indels: 1
DB: 9 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-777-564-697 (1-205)
QY 142 CysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIle 161
Db 4 TGCTCCAGCATCACTATCTCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCTCGCGTGTGTC 63
QY 162 ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGlyAsp 181
Db 64 ACCAACACATGATGTGCTGGACTG---GACCGGGGCCAGGACCCCTGCCACAGTGAC 120
QY 182 SerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAsp 201
Db 121 TCTGAGGSCCCCTGGCCTGTGACGAGACCCCTCCAGGACATCTCTCTGTGGGGTGTTC 180
QY 202 ProCysAlaIleThrArgLysPro 209
Db 181 CCCTGTGGCTCTGCCACGACATCCA 204

RESULT 4
US-10-015-219-697
; Sequence 697, Application US/10015219
; Publication No. US20030008299A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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Alignment Scores:

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; OTHER INFORMATION: EST_HUMAN HIT: BG762809.1, EVALUAE 3.00e-77
US-10-029-386-19717

Alignment Scores:
Pred. No.: 7.46e-08 Length: 147
Score: 138.50 Matches: 27
Percent Similarity: 66.67% Conservative: 5
Best Local Similarity: 56.25% Mismatches: 11
Query Match: 11.01% Indels: 5
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-19717 (1-147)

Qy 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGlyLe 195
Db 1 GGTGATTCGGGGGACCTCTGACCTGCTGCAGCTCGGAGCTGGTCTGGTGGGGTG 60
Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysVal 215
Db 61 GTGAGCTGGGCAAGGGT--TGTGCTCTGCCCAACGCTCCAGGGGTCTACACCAAGTGTG 11
Qy 216 CysLysTyrValAspTrpIleGln 223
Db 118 GCCACATATAGCCCTGGATTGAG 141

RESULT 14
US-10-344-394-20
; Sequence 20, Application US/10344394
; Publication No. US20040058342A1
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OF INVENTION: NOVEL KALLIKREIN GENE
; FILE REFERENCE: 11757.51USWO
; CURRENT APPLICATION NUMBER: US/10/344,394
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/CA01/01141
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,853
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 137
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-344-394-20

Alignment Scores:
Pred. No.: 1.36e-07 Length: 137
Score: 136.00 Matches: 23
Percent Similarity: 70.45% Conservative: 8
Best Local Similarity: 52.27% Mismatches: 13
Query Match: 10.81% Indels: 0
DB: 13 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-344-394-20 (1-137)

Qy 136 LeuProHisThrLeuArgCysAlaAsnIleThrIleLeuGlnHisGlnLysCysGlnAsn 155
Db 6 CTCCAGATACGTTGCATTGTGCCAACATCAGCATTTATCTCGACACATCTTTGTGCAAG 65
Qy 156 AlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLys 175
Db 66 AGCTACCCAGGGCGCTGACAAACACCATGTGTGTGTCAGGGCGGAGGGCAGAGCCGCA 125
Qy 176 AspSerCysGln 179
Db 126 GAATCTGTGAG 137

RESULT 15
US-09-867-701-3234/c
; Sequence 3234, Application US/09867701

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; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3234
; LENGTH: 163
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-3234

Alignment Scores:
Pred. No.: 1.73e-07 Length: 163
Score: 136.00 Matches: 25
Percent Similarity: 64.81% Conservative: 10
Best Local Similarity: 46.30% Mismatches: 19
Query Match: 10.81% Indels: 0
DB: 9 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-867-701-3234 (1-163)
QY 176 AspSerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 195
Db 163 AACTCTCCAGGGAATTCGGGGCTTGTGCTCTCAATGGCTCTCGCAAGGGAACCC 104
QY 196 IleSerTrpGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 103 GTGCTCTGGGATATTACCTTGTGGCCGCCCAACAGACCGGTTTCTACAGAACCTC 44
QY 216 CysLysTyrrValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 43 TGCAAGTTCACCAAGTGGATCCAGGAACCATCCAGGCCAAC 2

RESULT 16
US-09-856-320A-2_COPY_54_282 (1-229) x US-09-867-701-3234 (1-163)
; Sequence 16, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2000-06-21
; PRIOR FILING DATE: 2000-10-31
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-424-836-16

Alignment Scores:
Pred. No.: 8.98e-07 Length: 216
Score: 131.50 Matches: 25
Percent Similarity: 61.11% Conservative: 8
Best Local Similarity: 46.30% Mismatches: 16
Query Match: 10.45% Indels: 5
DB: 13 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-424-836-16 (1-216)
QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGlyIle 195
Db 1 GGTGACTCAGGTGGACCCCTTGGTCTGTGACAGGATCGGACTGTGGTATCAGGTGGAAATC 60
QY 196 IleSerTrpGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 61 GTGAGCTGGGGAATGGAC---TGGGGTCAACCAATCGGCTGTGTCTACACCAACATC 117
QY 216 CysLysTyrrValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 118 AGTGTGTACTTCCACTGGATCCGGAGGGTGTATGCCACAGT 159

RESULT 17
US-10-424-836-16
; Sequence 16, Application US/10424836
; Publication No. US20030224430A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/10/424,836
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/885,441
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-424-836-16

Alignment Scores:
Pred. No.: 8.98e-07 Length: 216
Score: 131.50 Matches: 25
Percent Similarity: 61.11% Conservative: 8
Best Local Similarity: 46.30% Mismatches: 16
Query Match: 10.45% Indels: 5
DB: 13 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-424-836-16 (1-216)
QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGlyIle 195
Db 1 GGTGACTCAGGTGGACCCCTTGGTCTGTGACAGGATCGGACTGTGGTATCAGGTGGAAATC 60
QY 196 IleSerTrpGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 61 GTGAGCTGGGGAATGGAC---TGGGGTCAACCAATCGGCTGTGTCTACACCAACATC 117
QY 216 CysLysTyrrValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 118 AGTGTGTACTTCCACTGGATCCGGAGGGTGTATGCCACAGT 159

RESULT 18
US-10-029-386-23119/c
; Sequence 23119, Application US/10029396
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.

```

```
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23119
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: NT HIT: M38193.1, EVALUE 1.00e-81
; OTHER INFORMATION: SWISSPROT HIT: P10144, EVALUE 1.00e-23
; OTHER INFORMATION: EST_HUMAN HIT: BF221604.1, EVALUE 3.00e-80
US-10-029-386-23119

Alignment Scores:
Pred. No.: 9.79e-07 Length: 154
Score: 129.50 Matches: 26
Percent Similarity: 69.39% Conservatives: 8
Best Local Similarity: 53.06% Mismatches: 12
Query Match: 10.29% Indels: 3
DB: 15 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-23119 (1-154)

QY 179 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlylleSerTrp 198
Db 153 CAGGGGACTCTGGAGCCCTTGTGTGTACACAGGTGGCCAGGGCATTGTCTCTAT 94
QY 199 GlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyr 218
Db 93 GGACGAAACAAT-----GCATGCTCCAGAGCTGCACCAAAAGTCTCAAGCTTT 43
QY 219 ValAspTrpIleGlnGluThrMetLys 227
Db 42 GTACACTGGATAAAGAAACCATGAAA 16

RESULT 19
US-10-029-386-23582
; Sequence 23582, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23582
; LENGTH: 216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
; OTHER INFORMATION: SWISSPROT HIT: P10323, EVALUE 2.00e-29
; OTHER INFORMATION: EST_HUMAN HIT: B1831427.1, EVALUE 1.00e-114
; OTHER INFORMATION: NT HIT: M77381.1, EVALUE 1.00e-103
US-10-029-386-23582

Alignment Scores:
Pred. No.: 2.07e-06 Length: 216
Score: 128.50 Matches: 26
Percent Similarity: 59.32% Conservatives: 9
Best Local Similarity: 44.07% Mismatches: 17
Query Match: 10.21% Indels: 7
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-23582 (1-216)

QY 177 SerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGln----- 193
Db 36 TCTGGACAGGGAGACAGCGGGGCCCTCTCATGTGAAACACACAGCAAGGAGGCGCTAT 95
QY 194 -----GlylleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGly 210
Db 96 GTGTCCTGGGAATCACAGCTGGGGGTAGGC---TGTGCCGTGCCAAGCGCCCGGA 152
QY 211 ValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 153 ATCTACACGGCCACCTGGCCCTATCTGACTGGATCGCTCCCAAGATTGTTCTTAAC 209

RESULT 20
US-10-029-386-23379
; Sequence 23379, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23379
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: SWISSPROT HIT: P50342, EVALUE 1.00e-19
; OTHER INFORMATION: EST_HUMAN HIT: BG953129.1, EVALUE 5.00e-92
; OTHER INFORMATION: NT HIT: AF23563.3, EVALUE 5.00e-97
US-10-029-386-23379

Alignment Scores:
Pred. No.: 4.9e-06 Length: 180
Score: 124.50 Matches: 25
Percent Similarity: 65.31% Conservatives: 7
Best Local Similarity: 51.02% Mismatches: 12
Query Match: 9.90% Indels: 5
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-23379 (1-180)

QY 179 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGly 194
Db 9 CAGGACGACTCCGGGGGGCCCTCTGTCTCCAGTGACGGTGGTGGTGGCTGGC 68
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PRIOR FILING DATE: 2000-04-07

Qy 20 ---GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThr 38
Db 94 GTGCCAGGCGCCCTTCCCTGTCGGAGGCGCCCTGCTTTCAGGCCAGTGGTCACTACT 153
Qy 39 AlaAlaHisCys 42
Db 154 GCTGCTCACTGC 165

RESULT 24
US-10-029-386-26364
; Sequence 26364, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOmica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26364
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: NT HIT: g114786995, EVALUE 1.00e-106
; OTHER INFORMATION: EST HUMAN HIT: BG656040.1, EVALUE 1.00e-106
; OTHER INFORMATION: SWISSPROT HIT: P06870, EVALUE 8.00e-33
US-10-029-386-26364

Alignment Scores:
Pred. No.: 1,11e-05 Length: 196
Score: 122.00 Matches: 26
Percent Similarity: 62.50% Conservative: 14
Best Local Similarity: 40.62% Mismatches: 16
Query Match: 9.70% Indels: 8
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-26364 (1-196)
Qy 73 ProHisProGlyPheAsnSerLeu-----ProknslyAsp 85
Db 3 CCACACCTGGCTTCAACATGAGCTCTCGAGAACACCCCGCCAGCAGCAGGAC 62
Qy 86 HisArgAsnAspIleMetLeuVallyMetAlaSerProVal---SerIleThrTrpAla 104
Db 63 TACAGCCACGACCTCATGCTGCTCGCCTGACAGAGCCTGCTGATACCATCACATGCT 122
Qy 105 ValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSer 124
Db 123 GTGAAGTCTGTGAGTGTGCCACCGAGGAACCCGAGTGGGGAGCACCCTGTTCCTTCC 182
Qy 125 GlyTrpGlySer 128
Db 183 GCGTGGGGCAGC 194

RESULT 25
US-10-029-386-21960
; Sequence 21960, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOmica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26364
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: NT HIT: g114786995, EVALUE 1.00e-106
; OTHER INFORMATION: EST HUMAN HIT: BG656040.1, EVALUE 1.00e-106
; OTHER INFORMATION: SWISSPROT HIT: P06870, EVALUE 8.00e-33
US-10-029-386-26364

FILE REFERENCE: AEOmica-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 21960
LENGTH: 149
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR19.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
OTHER INFORMATION: EST HUMAN HIT: W58737.1, EVALUE 2.00e-78
OTHER INFORMATION: NT HIT: g115301293, EVALUE 1.00e-78
OTHER INFORMATION: SWISSPROT HIT: P49862, EVALUE 4.00e-25
US-10-029-386-21960

Alignment Scores:
Pred. No.: 1,74e-05 Length: 149
Score: 119.00 Matches: 22
Percent Similarity: 59.52% Conservative: 3
Best Local Similarity: 52.38% Mismatches: 17
Query Match: 9.46% Indels: 0
DB: 15 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-21960 (1-149)
Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
Db 16 ATTATTGATGGCCGCCCTGTCGACAGAGCTCCACCCATGGCAGGTGGCCCTGCTCAGT 75
Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
Db 76 GGCATCAGCTCCACTGGGAGGCGCTCTGGTCAATGAGCGCTGGTCTCACTGCGGCC 135
Qy 41 HisCys 42
Db 136 CACTGC 141

RESULT 26
US-10-094-507-21
; Sequence 21, Application US/10094507
; Publication No. US20030143553A1
; GENERAL INFORMATION:
; APPLICANT: Sommer, Steve S.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION WITH DIRECT SEQUENCING
; FILE REFERENCE: 27709-A2AA
; CURRENT APPLICATION NUMBER: US/10/094,507
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Replication segment
; NAME/KEY: CDS
; LOCATION: (1)..(180)
; OTHER INFORMATION:
US-10-094-507-21

Alignment Scores:
Pred. No.: 3,96e-05 Length: 180
Score: 117.00 Matches: 20
Percent Similarity: 56.67% Conservative: 14
Best Local Similarity: 33.33% Mismatches: 24


```
Db 118 GAGAAAAGTGAAGCTTCTACACACGTGTGGCGGTAGCTCATCGCCCGGACTGGGTT 59
Qy 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
Db 58 GTGACTGCCGCCACTGCATCTCGAGCTCTGGACCTACACAGGTGGTGTGGGGGAG 2

RESULT 29
US-10-060-036-3490
; Sequence 3490, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3490
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3490

Alignment Scores:
Pred. No.: 0.000102 Length: 195
Score: 114.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 9.06% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3490 (1-195)
Qy 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---Phe 19
Db 18 GTTGTCAATGGTGAGGATCGGTCGCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 77
Qy 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 78 GAGAAAAGTGAAGCTTCTACACACGTGTGGCGGTAGCTCATCGCCCGGACTGGGTT 137
Qy 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
Db 138 GTGACTGCCGCCACTGCATCTCGAGCTCTCGACCTACACAGGTGGTGTGGGTGAG 194

RESULT 30
US-10-060-036-3865
; Sequence 3865, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3865
; LENGTH: 214
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3865

Alignment Scores:
Pred. No.: 0.000116 Length: 214
Score: 114.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 9.06% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3865 (1-214)
Qy 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---Phe 19
Db 37 GTTGTCAATGGTGAGGATCGGTCGCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 96
Qy 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 97 GAGAAAAGTGAAGCTTCTACACACGTGTGGCGGTAGCTCATCGCCCGGACTGGGTT 156
Qy 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
Db 157 GTGACTGCCGCCACTGCATCTCGAGCTCTCGACCTACACAGGTGGTGTGGGTGAG 213

RESULT 31
US-10-060-036-3854/c
; Sequence 3854, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3854
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 93
; OTHER INFORMATION: n = A,T,C or G
US-10-060-036-3854

Alignment Scores:
Pred. No.: 0.000145 Length: 205
Score: 113.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 8.98% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3854 (1-205)
Qy 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---Phe 19
Db 178 GTTGTCAATGGTGAGGATCGGTCGCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 119
Qy 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 118 GAGAAAAGTGAAGCTTCTACACAGGTGGTGGGTGAGCTCATCGCCCGGACTGGGTT 59
Qy 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
```

Db 58 GTGACTGCCGCACTGCATCTCGAGGGATCTGACCTACCAGTGGTGTGGTGAG 2

RESULT 32

US-10-060-036-3798
; Sequence 3798, Application US/10060036
; Publication No. US20030073144A1

```

; GENERAL INFORMATION:
;
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lucdes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
;
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
;

```

FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

```

; SOFTWARE: FastSEQ for Windows Version 4.0

```

; SEQ ID NO 3798

; LENGTH: 181

TYPE: DNA
ORGANISM: Homo sapiens

US-10-050-035-3700
; ORGANISM: Homo sapiens

US-10-060-036-3798

Alignment Scores:

Alignment scores:
Pred. No.: 0.000161 Length:

freq: no.:	0.000101	Length
Score:	112.00	Matches

Percent Similarity: 61.02%

Best Local Similarity: 40.68%

Query Match: 8.90%

DB: 15 Gaps: 15

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-

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1 IleIleLysGlypHeGluCysLysProHis
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4 GTTGTCCATGGTGAGGATGCGGTCCTACAT

Q11 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049

QY 20 GRLYSINRARGLEULEU-----CYSQ

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Qy 179 GlnGlyAspSerGlyGlyProLeuValCysHsnglnSer-----LeuGlnGly 194
Db 1 CAGGGTGACTCAGGTGGACCTTGGTCTGTGCACAAGGATGACGTGTGTATCAGGTTGGA 60
Qy 195 IleIleSerTPGlyGlnAspProCysAlaIleThrArgLysProGlyValTyThrLys 214
Db 61 ATCGTGAGCTGGGATGGAC---TGGCGTCAACCCATCGGCTGGTGTCTACACCAAC 117
Qy 215 Val 215
Db 118 ATC 120

RESULT 35
US-10-060-036-4110
; Sequence 4110, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Datin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4110
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4110

Alignment Scores:
Pred. No.: 0.000354 Length: 175
Score: 109.00 Matches: 24
Percent Similarity: 60.34% Conservative: 11
Best Local Similarity: 41.38% Mismatches: 17
Query Match: 8.66% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-4110 (1-175)

Qy 2 IleLysGlyPheGluCysLysProHisserGlnProTtpGlnAlaAlaLeu---PheGlu 20
Db 1 GTCCATGGTGAGGATGGCGTCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTATGAG 60
Qy 21 LysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeuLeu 37
Db 61 AAAAGTGAAGCTTCTACACACAGTGTGGCGGTAGCTCATCGCCCGCGANTGGGTTGTG 120
Qy 38 ThrAlaAlaHisCysLeuLysPro-----ArgTyIleValHisLeuGlyGln 53
Db 121 ACTGCGCGCACTGCATCTCGAGGATCTGACCTACCGAGGTGGTGTGGGTGAG 174

RESULT 36
US-10-060-036-3468
; Sequence 3468, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Datin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
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; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3468
; LENGTH: 218
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3468

Alignment Scores:
Pred. No.: 0.000481 Length: 218
Score: 109.00 Matches: 20
Percent Similarity: 65.96% Conservative: 11
Best Local Similarity: 42.55% Mismatches: 12
Query Match: 8.66% Indels: 4
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3468 (1-218)

Qy 1 IleIleLysGlyPheGluCysLysProHisserGlnProTtpGlnAlaAlaLeu---Phe 19
Db 77 GTTGTCATGGTGAGGATGGCGTCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 136
Qy 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 137 GAGAAAAGTGAAGCTTCTACACACAGTGTGGCGGTAGCTCATCGCCCGCGATTGGGT 196
Qy 37 LeuThrAlaAlaHisCysLeu 43
Db 197 GTGACTGCGCGCCACATGCAATC 217

RESULT 37
US-09-864-761-27190
; Sequence 27190, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1 GENE EXPRESSION ANALYSIS BY MICROARRAY
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,667
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 27190
 ; LENGTH: 175
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; OTHER INFORMATION: MAP TO AL078474.2
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
 ; OTHER INFORMATION: NT HIT: Y19139.1, EVALUE 6.00e-86
 ; OTHER INFORMATION: EST HUMAN HIT: BE737932.1, EVALUE 1.00e-85
 ; OTHER INFORMATION: SWISSPROT HIT: P98073, EVALUE 6.00e-30
 US-09-864-761-27190

Alignment Scores:
 Pred. No.: 0.000468 Length: 175
 Score: 108.00 Matches: 19
 Percent Similarity: 65.12% Conservative: 9
 Best Local Similarity: 44.19% Mismatches: 15
 Query Match: 8.59% Indels: 0
 DB: Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-864-761-27190 (1-175)

QY 1 IleilelysglyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
 Db 42 ATTGTCGAGAGTAATGCCAAGAGGGCGCTGCCCTGGTTCGTGATATAT 101
 QY 21 LyThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuThrAla 40
 Db 102 GCGGCGCGACTGCTGCGCGCATCTCTCGTCAGCAGTCACTGGTGTGTCGCCGCA 161
 QY 41 HisCysLeu 43
 Db 162 CACTGCGTG 170

RESULT 38
 US-09-923-779-118
 ; Sequence 118, Application US/09923779
 ; Patent No. US20020076721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.553
 ; CURRENT APPLICATION NUMBER: US/09/923,779
 ; CURRENT FILING DATE: 2001-08-06
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 118
 ; LENGTH: 220
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-923-779-118

Alignment Scores:
 Pred. No.: 0.000644 Length: 220
 Score: 108.00 Matches: 20
 Percent Similarity: 65.22% Conservative: 10
 Best Local Similarity: 43.48% Mismatches: 12
 Query Match: 8.59% Indels: 4
 DB: Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-118 (1-220)
 QY 1 IleilelysglyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
 Db 81 GTTGCAATGGTGAGGATGGGTCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 140
 QY 20 GlulysThrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
 Db 141 GAGAAAGTGGAAAGCTTCTACACACAGCTGTGGCGGTAGCCTCATCGCCCCCGATTGGTT 200
 QY 37 LeuThrAlaAlaHisCys 42
 Db 201 GTGACTCGCGGCCACTGC 218

RESULT 39
 US-09-923-779-119/c
 ; Sequence 119, Application US/09923779
 ; Patent No. US20020076721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.553
 ; CURRENT APPLICATION NUMBER: US/09/923,779
 ; CURRENT FILING DATE: 2001-08-06
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 119
 ; LENGTH: 220
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-923-779-119

Alignment Scores:
 Pred. No.: 0.000644 Length: 220
 Score: 108.00 Matches: 20
 Percent Similarity: 65.22% Conservative: 10
 Best Local Similarity: 43.48% Mismatches: 12
 Query Match: 8.59% Indels: 4
 DB: Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-119 (1-220)
 QY 1 IleilelysglyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
 Db 140 GTTGCAATGGTGAGGATGGGTCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 81
 QY 20 GlulysThrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
 Db 80 GAGAAAGTGGAAAGCTTCTACACACAGCTGTGGCGGTAGCCTCATCGCCCCCGATTGGTT 21
 QY 37 LeuThrAlaAlaHisCys 42
 Db 201 GTGACTCGCGGCCACTGC 3

RESULT 40
 US-09-923-779-124
 ; Sequence 124, Application US/09923779
 ; Patent No. US20020076721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.553
 ; CURRENT APPLICATION NUMBER: US/09/923,779
 ; CURRENT FILING DATE: 2001-08-06
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 124

```
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-779-124

Alignment Scores:
Pred. No.: 0.000644 Length: 220
Score: 108.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.59% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-124 (1-220)
QY 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
Db 81 GTTGTCATGTGGTGGAGTGGTCCCTACAGCTGGCCCTGGCAGGTTTCCTGCAGTAT 140
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeAlaProArgTrpLeu 36
Db 141 GAGAAAGTGGAGGCTTCTACACACAGTGTGGCGGTAGCCTCATCGCCCGGATTGGGTT 200
QY 37 LeuThrAlaAlaHisCys 42
Db 201 GTGACTGCGCGCCACTGC 218

RESULT 41
US-09-923-779-125/c
; Sequence 125, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-779-125

Alignment Scores:
Pred. No.: 0.000644 Length: 220
Score: 108.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.59% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-125 (1-220)
QY 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
Db 140 GTTGTCATGTGGTGGAGTGGTCCCTACAGCTGGCCCTGGCAGGTTTCCTGCAGTAT 81
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeAlaProArgTrpLeu 36
Db 80 GAGAAAGTGGAGGCTTCTACACACAGTGTGGCGGTAGCCTCATCGCCCGGATTGGGTT 21
QY 37 LeuThrAlaAlaHisCys 42
Db 201 GTGACTGCGCGCCACTGC 3

RESULT 42
US-09-923-779-126
; Sequence 126, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-779-126

Alignment Scores:
Pred. No.: 0.000644 Length: 220
Score: 108.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.59% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-126 (1-220)
QY 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
Db 81 GTTGTCATGTGGTGGAGTGGTCCCTACAGCTGGCCCTGGCAGGTTTCCTGCAGTAT 140
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeAlaProArgTrpLeu 36
Db 141 GAGAAAGTGGAGGCTTCTACACACAGTGTGGCGGTAGCCTCATCGCCCGGATTGGGTT 200
QY 37 LeuThrAlaAlaHisCys 42
Db 201 GTGACTGCGCGCCACTGC 218

RESULT 43
US-09-923-779-127/c
; Sequence 127, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-779-127

Alignment Scores:
Pred. No.: 0.000644 Length: 220
Score: 108.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.59% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-127 (1-220)
QY 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
Db 81 GTTGTCATGTGGTGGAGTGGTCCCTACAGCTGGCCCTGGCAGGTTTCCTGCAGTAT 140
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeAlaProArgTrpLeu 36
Db 141 GAGAAAGTGGAGGCTTCTACACACAGTGTGGCGGTAGCCTCATCGCCCGGATTGGGTT 200
QY 37 LeuThrAlaAlaHisCys 42
Db 201 GTGACTGCGCGCCACTGC 218
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Db 140 GTTCTCAATGGTGGAGGATGGCGTCCCTACAGCTGGCCCTGGCAGGTTCCCTCGCAGTAT 81
Qy 20 GlulysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 80 GAGAAAGTGAAGCTTCTACACACAGTGGCGGTAGCTCATCGCCCGGATGGGTT 21
Qy 37 LeuThrAlaAlaHisCys 42
Db 20 GTGACTCGCGCCACTGC 3

RESULT 44
US-10-029-386-14818/c
; Sequence 14818, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 14818
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR21 61.0
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: AL163285.2, EVALUE 1.00e-94
; OTHER INFORMATION: SWISSPROT HIT: O15393, EVALUE 1.00e-26
; OTHER INFORMATION: EST_HUMAN HIT: AA457407.1, EVALUE 7.00e-85
US-10-029-386-14818

Alignment Scores:
Pred. No.: 0.000543 Length: 176
Score: 107.50 Matches: 24
Percent Similarity: 57.69% Conservative: 6
Best Local Similarity: 46.15% Mismatches: 17
Query Match: 8.55% Indels: 5
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-14818 (1-176)
Qy 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGlyIle 195
Db 176 GGTGACAGTGGAGGCGCTCTGGTCACTCGAAGAACAAATATCTGGTGGCTGATAGGGAT 117
Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 116 ACAAGCTGGGTTCTTGGC---TGTGCAAAAGCTTACAGACAGGAGGTGTACGGGAATGTG 60
Qy 216 CysLysTyrValAspTrpIleGlnGluThrMetLys 227
Db 59 ATGGTATTACGAGCTGGATTTATCGACAAATGAGG 24

RESULT 45
US-10-029-386-26680
; Sequence 26680, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 14818
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR21 61.0
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: AL163285.2, EVALUE 1.00e-94
; OTHER INFORMATION: SWISSPROT HIT: O15393, EVALUE 1.00e-26
; OTHER INFORMATION: EST_HUMAN HIT: AA457407.1, EVALUE 7.00e-85
US-10-029-386-26680

Alignment Scores:
Pred. No.: 0.000543 Length: 176
Score: 107.50 Matches: 24
Percent Similarity: 57.69% Conservative: 6
Best Local Similarity: 46.15% Mismatches: 17
Query Match: 8.55% Indels: 5
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-26680 (1-176)
Qy 142 CysAlaAsnIleThrIleIleGluHisGlnCysGluAsnAlaTyrProGlyAsnIle 161
Db 3 TGCCTGGATGCTCGGTGCTGACCCAGCTGAGTGTAAAGCTCTTACCTCGAAAGATT 62
Qy 162 ThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGln 179
Db 63 ACCAACAGCATGTTCTGTGTGGGTTCTTCTTGAGGGAGGCAAGGATTCTGCGCAG 116

RESULT 46
US-09-923-779-89
; Sequence 89, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48, 49
; OTHER INFORMATION: n = A, T, C or G
US-09-923-779-89

Alignment Scores:
Pred. No.: 0.000787 Length: 208
Score: 107.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.51% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-89 (1-208)
```


Db 94 ACGRGTGGCGTAGCCTCATCGCCCGCGATTGGTTGTGACTGCGCGCCACTGCATCTCG 35
Qy 45 Pro-----ArgTyrIleValHisLeuGlyGln 53
Db 34 AGGATCTGACCTACCAAGTGGTGTGGGTGAG 2

RESULT 50

US-10-424-599-75219
; Sequence 75219, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 75219
; LENGTH: 189
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_38936C.1
US-10-424-599-75219

Alignment Scores:
Pred. No.: 0.00183 Length: 189
Score: 103.50 Matches: 26
Percent Similarity: 47.69% Conservative: 5
Best Local Similarity: 40.00% Mismatches: 25
Query Match: 8.23% Indels: 9
DB: Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-424-599-75219 (1-189)

Qy 162 ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGlyAsp 181
Db 2 TCTCAAAACATGTTCTGTGTGGACACCCATCTCTAAAGCAGGACGCTGCCAGGGGGAT 61
Qy 182 SerGlyGly-----ProLeuValCysAsnGlnSerLeuGlnGlyIle 195
Db 62 AGTGGGGCGGTTTTTGAGTAAGGACCCGACACTGATCGTGGTGGCCACGGGCATC 121
Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysVal 215
Db 122 GTGTCTCTGGGC-----ATCGGGTGCAGCAGGGGGCTATGGCTTCTACACCAAGTG 172
Qy 216 CysLysTyrValAsp 220
Db 173 CTCAACTACGTGGAC 187

Search completed: June 27, 2004, 00:33:00
Job time : 476 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2004, 23:38:31 ; Search time 434 Seconds
(without alignments)
2241.561 Million cell updates/sec

Title: US-09-856-320A-2_COPY_54_282

Perfect score: 1258

Sequence: 1 IIKGFECKPQNPQAALFE.....GVYTKVCKYVDWIOETMKN 229

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3849990

Minimum DB seq length: 0

Maximum DB seq length: 229

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

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-O=/cpn2.1/USPTO.spool/US09856320/runat_25062004_124554_1052/app_query.fasta_1.391
-PB=N_Geneseq_23Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MTN=0 -ALIGN=50
-MODE=LOCAL -OUTFMT=ptco -NORW=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=229
-USER=US09856320 @CGN 1 1 470 @runat_25062004_124554_1052 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04.*

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	206	16.4	153	6	Abk48915 Novel hum
2	202.5	16.1	205	4	Aae24516 Human ova
3	194	15.4	178	7	Ada05697 Human NOV
4	188	14.9	198	3	Aaz95014 Prostate
5	187	14.9	220	6	ABN17410 Human ORF
6	169	13.4	196	5	ABV33773 Human pro
7	169	13.4	196	5	ABV42670 Human pro
8	168	13.4	200	2	AAV60379 mRNA targ

9	164	13.0	154	6	ABK48905	Abk48905 Novel hum
10	164	13.0	216	6	ABK30236	Human G-p
11	163.5	13.0	202	6	ABN89908	Mouse cto
12	150	11.9	207	2	AAT40842	Serine pr
13	150	11.9	207	4	AAC90850	Flea seri
14	149.5	11.9	203	7	ABX46133	Bovine ES
15	147	11.7	208	2	AAT92975	CDNA for
16	147	11.7	225	2	AAT40854	Serine pr
17	147	11.7	225	2	AAT40854	Flea seri
18	147	11.7	225	4	AAC90862	Flea seri
19	146	11.6	218	2	AAT40847	Serine pr
20	146	11.6	218	2	AAV04590	Flea seri
21	146	11.6	218	4	AAC90855	Flea seri
22	136	10.8	137	6	ABK48911	Novel hum
23	136	10.8	153	6	ABL80256	Human ova
24	135	10.7	225	2	AAQ31930	Human scu
25	134.5	10.7	227	2	AAV57985	Human BS2
26	132	10.5	180	3	AAZ89009	Rat Facto
27	131	10.4	180	3	AAZ89011	Rabbit Fa
28	130	10.3	180	3	AAZ89008	Murine Fa
29	128	10.2	180	3	AAZ89010	Cavea sp.
30	127	10.1	176	5	ABV38446	Human pro
31	123.5	9.8	159	6	ABK30380	Human G-p
32	123	9.8	178	6	ABA92483	DNA oligo
33	123	9.8	178	6	ABA01120	Human PSA
34	123	9.8	178	6	ABSS2622	Human DNA
35	123	9.8	178	7	ABZ59354	Loop-medi
36	121	9.6	180	3	AAZ89012	Sheep Fac
37	120.5	9.6	179	5	ABV38147	Human pro
38	120.5	9.6	179	5	ABV44351	Human pro
39	117	9.3	172	8	AAZ8752	Human tra
40	117	9.3	180	3	AAZ89007	Human Fac
41	116	9.2	172	8	AAZ8758	Human tra
42	115	9.1	162	4	AAI53283	Probe #21
43	115	9.1	162	4	AAK47449	Human bon
44	115	9.1	162	4	AAK21293	Human bra
45	115	9.1	162	4	ABV37886	Human liv
46	114	9.1	184	6	ABV97886	Human liv
47	114	9.1	195	6	ABV98082	Human pan
48	114	9.1	214	6	ABV98457	Human pan
49	113	9.0	94	3	AAA64312	PCR pimer
50	113	9.0	205	6	ABV98446	Human pan
51	113	9.0	222	4	AAZ14836	Human PSI
52	112	8.9	181	6	ABV98390	Human pan
53	111.5	8.9	93	3	AAA64311	PCR pimer
54	109	8.7	175	6	ABV98702	Human pan
55	109	8.7	218	6	ABV98060	Human pan
56	108	8.6	175	4	AAK17832	Human bra
57	108	8.6	220	6	ABK44185	CDNA #125
58	108	8.6	220	6	ABK44184	CDNA #124
59	108	8.6	220	6	ABK44186	CDNA #126
60	108	8.6	220	6	ABK44178	CDNA #118
61	108	8.6	220	6	ABK44187	CDNA #127
62	108	8.6	220	6	ABK44179	CDNA #119
63	107	8.5	208	6	ABK44149	CDNA #89
64	105.5	8.4	192	2	AAT40841	Serine pr
65	105.5	8.4	192	4	AAC90849	Flea seri
66	105	8.3	156	6	ABV98175	Human pan
67	104.5	8.3	138	6	ABK31801	DNA encod
68	104	8.3	157	6	ABV97961	Human pan
69	103	8.2	226	2	AAQ33009	Human scu
70	101.5	8.1	116	4	AAI20964	Probe #10
71	101.5	8.1	116	4	ABK66033	Human foe
72	101.5	8.1	116	4	AAI46211	Probe #14
73	101.5	8.1	116	4	ABK48157	Human bre
74	101.5	8.1	116	4	ABA33118	Probe #11
75	101.5	8.1	116	4	AAK40196	Human bon
76	101.5	8.1	116	4	AAK14457	Human bra
77	101.5	8.1	116	4	ABV339776	Human liv
78	101.5	8.1	116	5	AAI06677	Probe #66
79	101.5	8.1	116	5	ABV33773	Human pro
80	101	8.0	216	6	ABK30257	Human G-p
81	101	8.0	224	7	ABV74948	Nucleotid

82	99	7.9	162	8	AAD58766	Human tra	155	80	6.4	200	6	AAD37038	Targettin
83	98.5	7.8	155	2	AAT13998	Mouse p6-	156	79	6.3	142	6	ABL63338	Breast ca
84	98.5	7.8	155	2	AAT03747	L37 conse	157	79	6.3	142	6	ABL65239	Lung canc
85	98.5	7.8	155	3	AA52250	Mouse pre	158	79	6.3	142	6	ABL64712	Lung canc
86	98.5	7.8	155	3	AA59705	Mouse bod	159	79	6.3	142	6	ABL62036	Colon ade
87	98.5	7.8	155	8	ACD13607	Mouse cdn	160	79	6.3	142	6	ABL6304	Lung canc
88	98.5	7.8	197	6	AKJ5330	Human air	161	79	6.3	181	6	ABL6733	Epithelin
89	98	7.8	77	2	AAQ63787	Bovine tr	162	79	6.3	186	2	AAK16733	Serine pr
90	98	7.8	211	6	ABK44076	cdNA #16	163	79	6.3	186	4	AAQ90831	Flea seri
91	96	7.6	65	6	ABN53102	Mouse spl	164	78	6.2	61	6	ABQ78140	Synthetic
92	95.5	7.6	155	2	AAQ03776	Mouse p6-	165	78	6.2	168	2	AAT40827	Serine pr
93	95.5	7.6	155	3	AA59705	Mouse p6-	166	78	6.2	168	2	AAC90832	Flea seri
94	95.5	7.6	155	8	ACD13608	Mouse p6-	167	77.5	6.2	159	2	AAT40823	Serine pr
95	95.5	7.6	169	6	AAD58763	Human tra	168	77.5	6.2	159	4	AAC90828	Flea seri
96	95	7.6	90	6	ABQ78147	Synthetic	169	77	6.1	96	3	AAA64304	PCR pimer
97	95	7.6	168	2	AAT40824	Serine pr	170	76.5	6.1	124	6	AAD29820	Human EST
98	95	7.6	168	4	AAC90829	Flea seri	171	76	6.0	63	2	AAT58862	Oligomer
99	95	7.6	172	4	ABA73267	Human foe	172	76	6.0	65	6	ABN28524	Rat splc
100	95	7.6	172	4	ABA73252	Human foe	173	76	6.0	65	6	ABN28537	Rat splc
101	95	7.6	172	4	AAI52965	Human foe	174	76	6.0	65	6	ABN53099	Mouse spl
102	95	7.6	172	4	AAK47129	Human bon	175	76	6.0	200	3	AAA64308	PCR pimer
103	95	7.6	172	4	AAK47869	Human bon	176	76	6.0	200	7	AAAD48774	3' target
104	95	7.6	172	4	AAK20976	Human bra	177	76	6.0	227	6	ABV98147	Human pan
105	95	7.6	172	4	AAK31703	Human bra	178	75.5	6.0	156	4	AAAL26333	Human bre
106	95	7.6	172	4	ABSA7587	Human liv	179	75.5	6.0	168	4	AAAL19283	Human bre
107	93	7.4	137	8	AAD58760	Human tra	180	75.5	6.0	217	4	AAAL19398	Human bre
108	92.5	7.4	219	4	AAK4532	Mouse dex	181	75	6.0	69	8	ACC85430	Chymotryp
109	92	7.3	60	6	ABN35820	Human spl	182	75	6.0	80	2	AAK23293	TR1 PCR
110	92	7.3	134	6	ABA90277	Human ORF	183	75	6.0	127	3	AAK93911	Cat flea
111	92	7.3	162	2	AAT40829	Serine pr	184	75	6.0	164	4	AAAL19327	Human bre
112	92	7.3	162	2	AAV04592	Flea seri	185	74	5.9	61	2	AAK52453	Reverse p
113	92	7.3	162	4	AAC90834	Flea seri	186	74	5.9	61	3	AAA46916	PCR prime
114	91	7.2	90	2	AAV58593	Prostate	187	74	5.9	61	3	ADC78594	Human PRO
115	91	7.2	90	2	AAV61208	cdNA sequ	188	74	5.9	61	4	AAK72611	Human PRO
116	91	7.2	90	3	AAA06356	Human imm	189	74	5.9	61	7	ACA59129	Human PRO
117	91	7.2	90	3	ABS71261	Human pro	190	74	5.9	61	7	ACA58526	PCR prime
118	91	7.2	90	4	AAH93472	Human pro	191	74	5.9	61	7	ACA60233	Human sec
119	91	7.2	90	4	AAH93472	Human pro	192	74	5.9	61	7	ACD07633	Novel hum
120	91	7.2	90	4	AAH02537	Prostate	193	74	5.9	61	7	ABX71681	Human sec
121	91	7.2	90	4	AAH84786	Human pro	194	74	5.9	61	7	ACH07013	Human sec
122	91	7.2	90	5	ACA59373	Prostate	195	74	5.9	61	7	ABX96250	Human sec
123	91	7.2	90	5	AA510115	Human pro	196	74	5.9	61	7	ACA05571	Human sec
124	91	7.2	90	6	ABL94936	Human P10	197	74	5.9	61	7	ACD20238	Human sec
125	91	7.2	90	6	ABS58645	Prostate	198	74	5.9	61	8	ACA55041	Novel sec
126	91	7.2	90	6	ACC95100	Prostate	199	74	5.9	61	8	ACD19876	Human sec
127	91	7.2	90	9	ADB13570	Human pro	200	74	5.9	61	8	ADB29487	Human sec
128	90.5	7.2	200	6	ABQ75507	Murine tr	201	74	5.9	61	8	ADA18343	Human sec
129	90	7.2	57	6	ABQ78145	Synthetic	202	74	5.9	61	8	ACD67023	Human sec
130	90	7.2	147	3	AAK93919	Cat flea	203	74	5.9	61	8	ACD83184	Human PRO
131	89	7.1	137	8	AAD58755	Human tra	204	74	5.9	61	8	ADA16318	Human sec
132	88	7.0	74	2	AAQ33790	Bovine tr	205	74	5.9	61	8	ADA42463	Human sec
133	87.5	7.0	116	2	AAQ31931	Human scu	206	74	5.9	61	8	ACD23362	Human PRO
134	87	6.9	93	2	AAQ63782	Bovine tr	207	74	5.9	61	8	ADA16742	Human sec
135	86	6.8	100	4	AAH02409	Human fac	208	74	5.9	61	8	ADA13171	Human sec
136	86	6.8	135	6	ABK31800	DNA encod	209	74	5.9	61	8	ADA42039	Human sec
137	85	6.8	60	2	AAT89214	Prostate	210	74	5.9	61	8	ADA17386	Human sec
138	85	6.8	77	2	AAQ63786	Bovine tr	211	74	5.9	61	8	ADA42889	Human sec
139	85	6.8	100	4	AAH02410	Human fac	212	74	5.9	61	8	ACD23724	Human PRO
140	85	6.8	168	2	AAT40820	Serine pr	213	74	5.9	61	8	ADB77808	Human sec
141	85	6.8	168	4	AAC90825	Flea seri	214	74	5.9	61	9	ADB74944	Human sec
142	84	6.7	137	8	AAD58765	Human tra	215	74	5.9	61	9	ADC28590	Human sec
143	84	6.7	164	5	ABV35541	Human pro	216	74	5.9	61	9	ADC3790	Human sec
144	84	6.7	193	6	ABV98322	Human pan	217	74	5.9	61	9	ADC40304	Human sec
145	83.5	6.6	200	6	AAD37041	Targettin	218	74	5.9	61	9	ADC19128	Human sec
146	83	6.6	107	5	ABQ78144	Synthetic	219	74	5.9	61	9	ADC34428	Human sec
147	83	6.6	107	5	ABV08544	Human pro	220	74	5.9	61	9	ADC29483	Human sec
148	83	6.6	137	7	ABQ83346	KLK4 alte	221	74	5.9	61	9	ADC29014	Human sec
149	83	6.6	200	6	AAD37040	Targettin	222	74	5.9	61	9	ADC40899	Human sec
150	82.5	6.6	220	6	ABK30330	Human G-p	223	74	5.9	61	9	ADC19556	Human sec
151	82	6.5	193	6	ABV97917	Human pan	224	74	5.9	61	9	ADC34004	Human sec
152	81.5	6.5	229	5	AA505418	Mammalian	225	74	5.9	61	9	ADC13074	Human sec
153	81	6.4	74	2	AAQ63791	Bovine tr	226	74	5.9	61	9	ADC12526	Human sec
154	80.5	6.4	76	2	AAQ63788	Bovine tr	227	74	5.9	61	9	ADD05081	Human sec

228	74	5.9	61	9	ADD04087	Abd04087 Human sec	301	60	4.8	65	6	ABN28495	Abn28495 Rat splc
229	74	5.9	61	9	ADD03663	Abd03663 Human sec	302	60	4.8	92	3	AAA64313	Aaa64313 PCR pimer
230	74	5.9	61	9	AD34915	Abd34915 Human sec	303	60	4.8	179	3	ABL23657	AbL23657 Drosophil
231	74	5.9	61	10	AD379360	Abd79360 Human sec	304	60	4.8	227	3	AAZ49262	Aaz49262 Human hyd
232	74	5.9	61	10	AD379784	Abd79784 Human sec	305	60	4.8	229	2	AAZ41399	Aaz41399 Human nor
233	74	5.9	61	10	AD373460	Abd73460 Human sec	306	59.5	4.7	119	2	AAZ52454	Aaz52454 Probe use
234	74	5.9	61	10	AD373995	Abd73995 Human sec	307	59.5	4.7	119	3	AAA46917	Aaa46917 Probe use
C 235	74	5.9	143	4	ABA72967	AbA72967 Human foe	308	59.5	4.7	119	3	AD378595	Adc78595 Human PRO
C 236	74	5.9	143	4	AAI53391	Abi53391 Probe #22	309	59.5	4.7	119	3	Aaf72612	Aaf72612 Human PRO
C 237	74	5.9	143	4	AAK47559	Abk47559 Human bon	310	59.5	4.7	119	7	ACA59130	AcA59130 Human PRO
C 238	74	5.9	143	4	AAK21398	Abk21398 Human bra	311	59.5	4.7	119	7	ACA58527	AcA58527 Probe #50
C 239	74	5.9	143	4	AS472994	AbS472994 Human liv	312	59.5	4.7	119	7	ACA60234	AcA60234 Human sec
C 240	74	5.9	143	6	AS221654	AbS221654 Human gen	313	59.5	4.7	119	7	ACD07634	AdC07634 Novel hum
241	74	5.9	199	4	AAI08940	Abi08940 Human bre	314	59.5	4.7	119	7	ABX71682	AbX71682 Human sec
242	73	5.8	182	6	ABT06520	AbT06520 Human ser	315	59.5	4.7	119	7	ACH07014	AcH07014 Human sec
243	73	5.8	210	1	AA90785	Abn90785 Sequence	316	59.5	4.7	119	7	ABX96251	AbX96251 Human sec
244	73	5.8	210	3	AAZ89014	Abz89014 Human fac	317	59.5	4.7	119	7	ACA05572	AcA05572 Human sec
C 245	71.5	5.7	76	2	AAQ63789	Abq63789 Bovine tr	318	59.5	4.7	119	7	ACD20239	AdC20239 Human sec
C 246	71.5	5.7	93	2	AAQ63783	Abq63783 Bovine tr	319	59.5	4.7	119	7	ACA55042	AcA55042 Novel sec
247	71	5.6	51	4	AAI26842	Abi26842 Human SNP	320	59.5	4.7	119	8	ACD19877	AdC19877 Human sec
248	71	5.6	60	4	AAH03228	Abh03228 Human fac	321	59.5	4.7	119	8	ADB29488	AdB29488 Human sec
249	71	5.6	67	2	AAH78020	Abh78020 Chimeric	322	59.5	4.7	119	8	ADA18344	AdA18344 Human sec
250	71	5.6	214	1	AAH71331	Abh71331 Exon 3 hu	323	59.5	4.7	119	8	AD67024	AdD67024 Human sec
251	68	5.4	60	6	ABN35936	Abn35936 Human spl	324	59.5	4.7	119	8	ACD83185	AdC83185 Human PRO
252	68	5.4	65	6	ABN53220	Abn53220 Mouse spl	325	59.5	4.7	119	8	ADA16319	AdA16319 Human sec
253	68	5.4	200	6	AAI44661	Abi44661 Clr gene	326	59.5	4.7	119	8	ADA42464	AdA42464 Human sec
254	67.5	5.4	159	2	AAH40843	Abh40843 Serine pr	327	59.5	4.7	119	8	ACD23363	AdC23363 Human PRO
255	67.5	5.4	159	4	AAH90851	Abh90851 Flea seri	328	59.5	4.7	119	8	ADA16743	AdA16743 Human sec
C 256	67	5.3	36	6	AAH20774	Abh20774 Mutagenic	329	59.5	4.7	119	8	ADA13172	AdA13172 Human sec
C 257	66.5	5.3	206	2	AAQ06663	Abq06663 Synthetic	330	59.5	4.7	119	8	ADA42040	AdA42040 Human sec
C 258	66.5	5.3	217	2	AAQ06662	Abq06662 Synthetic	331	59.5	4.7	119	8	ADA17387	AdA17387 Human sec
C 259	66	5.2	81	2	AAQ63777	Abq63777 Bovine tr	332	59.5	4.7	119	8	ADA42890	AdA42890 Human sec
260	66	5.2	210	7	ACC49832	Abc49832 Human cyt	333	59.5	4.7	119	8	ACD23725	AdC23725 Human PRO
261	65.5	5.2	208	4	AAI09038	Abi09038 Human bre	334	59.5	4.7	119	9	ADB77809	AdB77809 Human sec
262	65	5.2	60	6	ABN35844	Abn35844 Human spl	335	59.5	4.7	119	9	ADB74945	AdB74945 Human sec
263	65	5.2	65	6	ABN53148	Abn53148 Mouse spl	336	59.5	4.7	119	9	ADC28591	AdC28591 Human sec
264	65	5.2	78	8	ACC85424	Abc85424 Chymotryp	337	59.5	4.7	119	9	ADC39791	AdC39791 Human sec
265	65	5.2	81	2	AAQ63776	Abq63776 Bovine tr	338	59.5	4.7	119	9	ADC19129	AdC19129 Human sec
266	65	5.2	150	2	AAQ49769	Abq49769 CAP37 pro	339	59.5	4.7	119	9	ADC34429	AdC34429 Human sec
267	65	5.2	156	2	AAH40819	Abh40819 Serine pr	340	59.5	4.7	119	9	ADC29484	AdC29484 Human sec
268	65	5.2	156	4	AAH90824	Abh90824 Flea seri	341	59.5	4.7	119	9	ADC29015	AdC29015 Human sec
269	65	5.2	203	4	AAH97749	Abh97749 Human gas	342	59.5	4.7	119	9	ADC40900	AdC40900 Human sec
C 270	64	5.1	91	2	AAH78018	Abh78018 Chimeric	343	59.5	4.7	119	9	ADC19557	AdC19557 Human sec
271	64	5.1	91	2	AAH78017	Abh78017 Chimeric	344	59.5	4.7	119	9	ADC34005	AdC34005 Human sec
272	64	5.1	120	2	AAH40828	Abh40828 Serine pr	345	59.5	4.7	119	9	ADC13075	AdC13075 Human sec
273	64	5.1	120	4	AAH90833	Abh90833 Flea seri	346	59.5	4.7	119	9	ADC12527	AdC12527 Human sec
274	64	5.1	136	7	ACC49841	Abc49841 Human rec	347	59.5	4.7	119	9	ADD05082	AdD05082 Human sec
275	64	5.1	197	2	AAV04603	Abv04603 Flea seri	348	59.5	4.7	119	9	ADD04088	AdD04088 Human sec
276	64	5.1	197	4	AAH90894	Abh90894 Flea seri	349	59.5	4.7	119	9	ADD03664	AdD03664 Human sec
C 277	64	5.1	219	5	AAH52279	Abh52279 Human App	350	59.5	4.7	119	9	ADE34916	AdE34916 Human sec
C 278	64	5.1	220	2	AAH9574	Abh9574 Human sec	351	59.5	4.7	119	10	ADE79361	AdE79361 Human sec
C 279	63	5.0	63	2	AAH58863	Abh58863 Oligomer	352	59.5	4.7	119	10	ADE79785	AdE79785 Human sec
C 280	63	5.0	88	2	AAH63785	Abh63785 Bovine tr	353	59.5	4.7	119	10	ADE73461	AdE73461 Human sec
281	62.5	5.0	72	8	ACC85431	Abc85431 Chymotryp	354	59.5	4.7	119	10	ADE73996	AdE73996 Human sec
282	62	4.9	39	2	AAV72614	Abv72614 Rat Facto	355	59.5	4.7	159	2	AAH40825	AdH40825 Serine pr
283	62	4.9	39	2	AAH209550	Abh209550 Rat Facto	356	59.5	4.7	159	4	AAH90830	AdH90830 Flea seri
284	62	4.9	88	2	AAQ63784	Abq63784 Bovine tr	357	59.5	4.7	168	6	ABN16422	Abn16422 Human ORF
285	62	4.9	100	3	AAH64309	Abh64309 PCR pimer	358	59.5	4.7	177	6	AAH40821	AdH40821 Serine pr
286	61.5	4.9	135	7	ACC49844	Abc49844 Human rec	359	59.5	4.7	177	4	AAH90826	AdH90826 Flea seri
287	61	4.8	60	6	ABN35858	Abn35858 Human spl	360	59.5	4.7	200	6	AAH44656	AdH44656 Ubiqutin
288	61	4.8	65	6	ABN28522	Abn28522 Rat splc	361	59	4.7	39	4	AAH29713	AdH29713 Murine fa
289	61	4.8	65	6	ABN53110	Abn53110 Mouse spl	362	59	4.7	39	4	AAH29712	AdH29712 Murine fa
290	61	4.8	152	2	AAH10848	Abh10848 Human bia	363	59	4.7	43	3	AAA37221	AAA37221 Human PRO
C 291	61	4.8	206	4	AAH53895	Abh53895 Murine tr	364	59	4.7	43	4	AAH54328	Aaf54328 Probe #28
292	61	4.8	207	6	ABV88239	Abv88239 Human col	365	59	4.7	43	8	ACD68365	AdC68365 Novel hum
293	61	4.8	228	2	AAH33746	Abh33746 Cellubrev	366	59	4.7	43	8	ACH04467	AcH04467 Human sec
294	61	4.8	228	3	AAH39892	Abh39892 Human cel	367	59	4.7	43	8	AD68011	AdD68011 Novel hum
295	61	4.8	228	3	AAH60722	Abh60722 Human cel	368	59	4.7	43	9	ADC18047	AdC18047 Human PRO
296	60.5	4.8	150	2	AAQ04061	Abq04061 Homologou	369	59	4.7	43	9	ADD70693	AdD70693 Human sec
C 297	60.5	4.8	196	9	ADD49332	AdD49332 Human lun	370	59	4.7	43	9	ADD39770	AdD39770 Human sec
C 298	60.5	4.8	222	6	ABH85865	Abh85865 Human ova	371	59	4.7	43	9	ADD70216	AdD70216 Human sec
C 299	60	4.8	51	4	AAH33111	Abh33111 Human SNP	372	59	4.7	43	9	ADD38337	AdD38337 Human sec
300	60	4.8	64	6	ABQ78134	Abq78134 Synthetic	373	59	4.7	43	9	ADD39293	AdD39293 Human sec

374	59	4.7	43	9	ADD38816	Human sec
375	59	4.7	43	9	ADD40247	Human sec
376	59	4.7	43	9	ADD50468	Human sec
377	59	4.7	43	9	ADD50468	Human sec
378	59	4.7	43	9	ADD50468	Human sec
379	59	4.7	43	9	ADD50468	Human sec
380	59	4.7	43	9	ADD50468	Human sec
381	59	4.7	43	9	ADD50468	Human sec
382	59	4.7	43	9	ADD50468	Human sec
383	59	4.7	43	9	ADD50468	Human sec
384	59	4.7	43	9	ADD50468	Human sec
385	59	4.7	43	9	ADD50468	Human sec
386	59	4.7	43	9	ADD50468	Human sec
387	59	4.7	43	9	ADD50468	Human sec
388	59	4.7	43	9	ADD50468	Human sec
389	58.5	4.7	119	3	AAK21698	Human sec
390	58.5	4.7	173	2	AAQ06661	Synthetic
391	58.5	4.7	184	2	AAQ06661	Synthetic
392	58	4.6	213	2	AAQ06661	Synthetic
393	58	4.6	213	2	AAQ06661	Synthetic
394	58	4.6	213	2	AAQ06661	Synthetic
395	58	4.6	219	2	AAQ06661	Synthetic
396	58	4.6	225	2	AAQ06661	Synthetic
397	57.5	4.6	201	2	AAQ06661	Synthetic
398	57.5	4.6	228	5	AAQ06661	Synthetic
399	57.5	4.6	229	2	AAQ06661	Synthetic
400	57.5	4.6	229	2	AAQ06661	Synthetic
401	57	4.5	39	2	AAQ06661	Synthetic
402	57	4.5	39	2	AAQ06661	Synthetic
403	57	4.5	59	6	AAQ06661	Synthetic
404	57	4.5	60	6	AAQ06661	Synthetic
405	57	4.5	65	6	AAQ06661	Synthetic
406	57	4.5	163	5	AAQ06661	Synthetic
407	57	4.5	186	4	AAQ06661	Synthetic
408	57	4.5	186	4	AAQ06661	Synthetic
409	57	4.5	189	6	AAQ06661	Synthetic
410	57	4.5	189	7	AAQ06661	Synthetic
411	57	4.5	189	7	AAQ06661	Synthetic
412	57	4.5	189	7	AAQ06661	Synthetic
413	57	4.5	189	7	AAQ06661	Synthetic
414	57	4.5	189	7	AAQ06661	Synthetic
415	57	4.5	189	7	AAQ06661	Synthetic
416	57	4.5	189	7	AAQ06661	Synthetic
417	57	4.5	189	7	AAQ06661	Synthetic
418	57	4.5	189	7	AAQ06661	Synthetic
419	57	4.5	189	7	AAQ06661	Synthetic
420	57	4.5	189	7	AAQ06661	Synthetic
421	57	4.5	189	7	AAQ06661	Synthetic
422	57	4.5	189	7	AAQ06661	Synthetic
423	57	4.5	189	7	AAQ06661	Synthetic
424	57	4.5	189	7	AAQ06661	Synthetic
425	57	4.5	189	7	AAQ06661	Synthetic
426	57	4.5	189	7	AAQ06661	Synthetic
427	57	4.5	189	7	AAQ06661	Synthetic
428	57	4.5	189	7	AAQ06661	Synthetic
429	57	4.5	189	7	AAQ06661	Synthetic
430	57	4.5	189	7	AAQ06661	Synthetic
431	56.5	4.5	189	7	AAQ06661	Synthetic
432	56.5	4.5	189	7	AAQ06661	Synthetic
433	56.5	4.5	189	7	AAQ06661	Synthetic
434	56.5	4.5	189	7	AAQ06661	Synthetic
435	56.5	4.5	189	7	AAQ06661	Synthetic
436	56.5	4.5	189	7	AAQ06661	Synthetic
437	56.5	4.5	189	7	AAQ06661	Synthetic
438	56	4.5	50	4	AAQ06661	Synthetic
439	56	4.5	64	2	AAQ06661	Synthetic
440	56	4.5	65	6	AAQ06661	Synthetic
441	56	4.5	146	6	AAQ06661	Synthetic
442	56	4.5	146	6	AAQ06661	Synthetic
443	56	4.5	159	6	AAQ06661	Synthetic
444	56	4.5	160	5	AAQ06661	Synthetic
445	56	4.5	173	4	AAQ06661	Synthetic
446	56	4.5	173	4	AAQ06661	Synthetic

C 447	56	4.5	173	4	AAK48795	Human bon
C 448	56	4.5	173	4	AAK48795	Human bon
C 449	56	4.5	173	4	AAK48795	Human bon
C 450	56	4.5	173	4	AAK48795	Human bon
C 451	56	4.5	200	6	AAK48795	Human bon
C 452	55.5	4.4	65	2	AAK48795	Human bon
C 453	55.5	4.4	125	2	AAK48795	Human bon
C 454	55.5	4.4	159	4	AAK48795	Human bon
C 455	55.5	4.4	159	4	AAK48795	Human bon
C 456	55.5	4.4	159	4	AAK48795	Human bon
C 457	55.5	4.4	159	4	AAK48795	Human bon
C 458	55.5	4.4	159	4	AAK48795	Human bon
C 459	55.5	4.4	159	4	AAK48795	Human bon
C 460	55.5	4.4	159	4	AAK48795	Human bon
C 461	55.5	4.4	159	4	AAK48795	Human bon
C 462	55.5	4.4	159	4	AAK48795	Human bon
C 463	55.5	4.4	159	4	AAK48795	Human bon
C 464	55.5	4.4	159	4	AAK48795	Human bon
C 465	55.5	4.4	173	3	AAK48795	Human bon
C 466	55.5	4.4	199	4	AAK48795	Human bon
C 467	55.5	4.4	199	4	AAK48795	Human bon
C 468	55.5	4.4	199	4	AAK48795	Human bon
C 469	55.5	4.4	199	4	AAK48795	Human bon
C 470	55.5	4.4	199	4	AAK48795	Human bon
C 471	55.5	4.4	199	4	AAK48795	Human bon
C 472	55.5	4.4	199	4	AAK48795	Human bon
C 473	55.5	4.4	199	4	AAK48795	Human bon
C 474	55.5	4.4	207	2	AAK48795	Human bon
C 475	55.5	4.4	207	2	AAK48795	Human bon
C 476	55.5	4.4	210	3	AAK48795	Human bon
C 477	55.5	4.4	210	3	AAK48795	Human bon
C 478	55.5	4.4	221	6	AAK48795	Human bon
C 479	55.5	4.4	222	6	AAK48795	Human bon
C 480	55	4.4	51	4	AAK48795	Human bon
C 481	55	4.4	51	4	AAK48795	Human bon
C 482	55	4.4	51	4	AAK48795	Human bon
C 483	55	4.4	51	4	AAK48795	Human bon
C 484	55	4.4	51	4	AAK48795	Human bon
C 485	55	4.4	51	4	AAK48795	Human bon
C 486	55	4.4	192	4	AAK48795	Human bon
C 487	55	4.4	192	4	AAK48795	Human bon
C 488	55	4.4	195	7	AAK48795	Human bon
C 489	55	4.4	198	4	AAK48795	Human bon
C 490	55	4.4	219	5	AAK48795	Human bon
C 491	55	4.4	222	6	AAK48795	Human bon
C 492	55	4.4	225	6	AAK48795	Human bon
C 493	55	4.4	226	9	AAK48795	Human bon
C 494	55	4.4	228	9	AAK48795	Human bon
C 495	54.5	4.3	132	3	AAK48795	Human bon
C 496	54.5	4.3	132	3	AAK48795	Human bon
C 497	54.5	4.3	212	3	AAK48795	Human bon
C 498	54	4.3	30	6	AAK48795	Human bon
C 499	54	4.3	30	6	AAK48795	Human bon
C 500	54	4.3	60	6	AAK48795	Human bon

ALIGNMENTS

RESULT 1

ABK48915
ID ABK48915 standard; DNA; 153 BP.

XX
AC ABK48915;
XX
DT 02-JUL-2002 (first entry)

XX Novel human kallikrein KLK15, intron 5.

XX Kallikrein; KLK15; cancer; prostate cancer; kidney cancer;
XX testicular cancer; thyroid disorder; chromosome 19q13.3-q13.4; ds.

XX Homo sapiens.

XX

PN WO200214485-A2.

XX 21-FEB-2002.

XX 10-AUG-2001; 2001WO-CA001141.

XX 11-AUG-2000; 2000US-0224853P.

XX (MOUN) MOUNT SINAI HOSPITAL.

XX Yousef GM, Diamandis BP;

XX WPI; 2002-329575/36.

XX Novel kallikrein protein, KLK15 and nucleic acid molecule encoding the

XX protein useful for diagnosing, monitoring and treating thyroid disorders

XX and cancer, particularly prostate, colon, kidney and testicular cancer.

XX Claim 3; Page 63; 67pp; English.

XX The invention describes an isolated kallikrein protein (I) (KLK15) and

XX splice variants of (I). (I) is useful for identifying a substance which

XX associates with (I) and for evaluating a compound for its ability to

XX modulate the biological activity of (I). An anti-(I) antibody labelled

XX with a detectable substance is useful to detect KLK15 polypeptide in

XX biological samples, tissues and cells. The antibody is also useful for

XX monitoring the progression of cancer in an individual. (I) and the

XX polynucleotide encoding it are useful for treatment of a condition

XX mediated by KLK15 protein, in particular cancer (including prostate,

XX colon, kidney and testicular cancer) and thyroid disorders. This sequence

XX (located on chromosome 19q13.3-q13.4) represents intron 5 of the gene

XX encoding the novel human kallikrein protein (see ABK48346) described in

XX the invention

XX Sequence 153 BP; 33 A; 38 C; 49 G; 33 T; 0 U; 0 Other;

XX SQ

Alignment Scores:

Pred. No.: 3.2e-10 Length: 153

Score: 206.00 Matches: 36

Percent Similarity: 80.00% Conservative: 4

Best Local Similarity: 72.00% Mismatches: 10

Query Match: 16.38% Indels: 0

DB: 6 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABK48915 (1-153)

QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 199

Db 1 GGTGACTCTGGGGGACCCCTGCTGTGGGGGCATCTTCGAGGCGATTGTCTCTGGGGT 60

QY 200 GlnAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrVal 219

Db 61 GACGTCCCTGTGTGACAAACACCAACCAAGCTGTGTCTATACCAAAAGTCTGCCACTTGT 120

QY 220 AspTyrIleGlnGluThrMetLysAsnAsn 229

Db 121 GAGTGTGATCAGGGAACCATGAAGAGGAAC 150

RESULT 2

ADA05697

ID AAS24516 standard; cDNA; 205 BP.

XX AAS24516;

XX 07-NOV-2001 (first entry)

XX Human ovarian PCR-subtracted cDNA library clone #697.

XX Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;

XX gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;

XX primer; probe.

XX Homo sapiens.

OS

XX WO200157207-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003733.

XX 04-FEB-2000; 2000US-0180403P.

XX 28-MAR-2000; 2000US-0192745P.

XX (CORI-) CORIXA CORP.

XX Algate PA, Mannion J;

XX WPI; 2001-488879/53.

XX New polynucleotides encoding ovarian tumor proteins, useful for treating

XX ovarian cancer, and as probes, primers, and markers of cancer

XX progression.

XX Example 1; Page 225; 378pp; English.

XX The invention comprises compositions used for the therapy and diagnosis

XX of ovarian cancer. The compositions comprise one or more ovarian tumour

XX proteins, their associated polynucleotides, or immunogenic portions of

XX the proteins. The ovarian tumour polynucleotides and polypeptides are

XX useful for stimulating and/or expanding T cells specific for a tumour

XX protein. They are also useful for inhibiting the development of cancer in

XX a patient with an ovarian tumour DNA or protein by incubating isolated T-

XX cells allowing them to proliferate, and administering to the patient. The

XX sequences can be used as markers for cancer, for example, to monitor

XX ovarian cancer progression. Probes and primers are useful in nucleic acid

XX hybridisation, in detecting the presence of complementary sequences in a

XX given sample, for preparing mutant species and for preparing other

XX genetic constructions. Sequences AAS23820-AAS25231 and AAS25238-AAS25549

XX represent human ovarian tumour protein cDNA clones

XX SQ Sequence 205 BP; 38 A; 67 C; 56 G; 44 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.62e-10 Length: 205

Score: 202.50 Matches: 34

Percent Similarity: 73.53% Conservative: 16

Best Local Similarity: 50.00% Mismatches: 17

Query Match: 16.10% Indels: 1

DB: 4 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAS24516 (1-205)

QY 142 CysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIle 161

Db 4 TGTCTCCAGCATCTATCTCTGAGCCCTAAGAGTGTGAGGTCTTCTACCTGGCGTGGTC 63

QY 162 ThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGlnGlyAsp 181

Db 64 ACCAACCAACATGATGTGTGTGGACTG---GACCGGGGCCAGGACCTTCCAGAGTGAC 120

QY 182 SerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAsp 201

Db 121 TCTGGAGGCCCCCTGGCCTGTGAGGAGACCTTCCAGGCAATCTCTCTGGGTGTTTAC 180

QY 202 ProCysAlaIleThrArgLysPro 209

Db 181 CCTGTGGCTCTGCCAGCATCCA 204

RESULT 3

ADA05697

ID ADA05697 standard; cDNA; 178 BP.

XX ADA05697;

XX 06-NOV-2003 (first entry)

XX

PN WO200023111-A1.
XX 27-APR-2000.
XX 19-OCT-1999; 99WO-US042331.
XX 19-OCT-1998; 98US-0104737P.
XX (DIAD-) DIADEXUS LLC.
XX Salceda S, Recipon H, Cafferkey R;
XX WPI; 2000-339531/29.
XX Diagnosing, staging and monitoring the presence and metastases of
XX prostate cancer especially useful for treating prostate cancer comprises
XX measuring changes in cancer specific gene levels.
XX Claim 7; Page 65; 74pp; English.
XX The present sequence is that of cancer specific gene (CSG) clone
XX 2626135H1, which was identified in a database search using the data
XX mining Cancer Leads Automatic Search Package (CLASP), which allows the
XX identification of highly expressed organ and cancer specific genes. The
XX invention provides ESs and full-length contigs for prostate CSGs (see
XX AA294998-295017). The CSGs, polypeptides encoded by them, and antibodies
XX that specifically bind CSG are used in new, claimed methods for
XX detecting, diagnosing, monitoring, staging, imaging and treating prostate
XX cancer. The new methods provide earlier diagnosis for the presence and
XX metastasis of prostate cancer, and can be used to determine if a cancer
XX has metastasized, or to monitor the progress or stage of the disease when
XX it has not metastasized
XX Sequence 198 BP; 39 A; 58 C; 60 G; 40 T; 0 U; 1 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.87e-08 Length: 198
XX Score: 188.00 Matches: 31
XX Percent Similarity: 70.59% Conservative: 10
XX Best Local Similarity: 53.45% Mismatches: 17
XX Query Match: 14.94% Indels: 0
XX DB: 3 Gaps:
XX
XX US-09-856-320A-2_COPY_54_282 (1-229) x AA295014 (1-198)
XX
XX QY 164 ThrMetValCysAlaSerValGlnGluGlyGlyValAspSerCysGlnGlyAspSerGly 183
XX Db 17 AGCATGTTCTGCGCGCGGAGGCGAAGACCCAGAGGACTCTTCGCAACGGTGACTCTGGG 76
XX
XX QY 184 GlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCys 203
XX Db 77 GGGCCCTGATCTGCAACGGGTACTTGCAGGCGCTTGTCGTTGCGAAAGCCCGTGT 136
XX
XX QY 204 AlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTrp 221
XX Db 137 GGCCCAAGTGGCGTCCAGGCTGTCTACCAACCTCTGCAAAATTCAGTGG 190
XX
XX RESULT 5
XX ABN17410
XX ID ABN17410 standard; cDNA; 220 BP.
XX XX
XX AC ABN17410;
XX XX
XX DT 24-JUN-2002 (first entry)
XX XX
XX DE Human ORFX polynucleotide sequence SEQ ID NO:3297.
XX XX
XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
XX degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX hyperextension; hypothyroidism; cholesterol ester storage disease;
XX immune deficiency; immune disorder; infectious disease;

KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis; gene; ss.
XX Homo sapiens.
XX WO200192523-A2.
XX 06-DEC-2001.
XX 29-MAY-2001; 2001WO-US010836.
XX 30-MAY-2000; 2000US-0206132P.
XX 29-AUG-2000; 2000US-0228716P.
XX (CURA-) CURAGEN CORP.
XX Shimkets RA, Leach MD;
XX WPI; 2002-106308/14.
XX P-PSDB; ABP01658.
XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders.
XX Disclosure; SEQ ID NO 3297; 1037pp; English.
XX The present invention describes substantially purified human proteins
XX (referred to as open reading frame, ORFX, where X is 1-11491 (see table 1
XX in the specification) ABN15762 to ABN27352 encode the human ORFX
XX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
XX treating or preventing a pathology associated with an ORFX-associated
XX disorder in humans, and in the manufacture of a medicament for treating a
XX syndrome associated with ORFX-associated disorder. ORFX polynucleotide
XX sequences can be used in gene therapy. ORFX sequences can be used in the
XX treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
XX psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
XX osteoarthritis, neurodegenerative disorders, disorders related to organ
XX transplantation, cardiovascular diseases, diabetes mellitus, systemic
XX lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
XX storage disease, various immune deficiencies and disorders, infectious
XX diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
XX arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
XX disease and autoimmune inflammatory eye disease. ORFX proteins are also
XX useful for treating burns, incisions, ulcers, for treating osteoporosis,
XX bone degenerative disorders, or periodontal disease, and for gut
XX protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues and conditions resulting from
XX systemic cytokine damage. N.B. The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 220 BP; 57 A; 68 C; 45 G; 49 T; 0 U; 1 Other;

XX Alignment Scores:
XX Pred. No.: 2.63e-08 Length: 220
XX Score: 187.00 Matches: 33
XX Percent Similarity: 67.65% Conservative: 13
XX Best Local Similarity: 48.53% Mismatches: 22
XX Query Match: 14.86% Indels: 0
XX DB: 6 Gaps:
XX
XX US-09-856-320A-2_COPY_54_282 (1-229) x ABN17410 (1-220)
XX
XX QY 10 HisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGlyAlaThr 29
XX Db 1 AAMTCCCAACCTGGCAAGTGGCTCTATACGCTTCAGCAATACTCTGCGGGGTGTC 60
XX
XX QY 30 LeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrpIleVal 49
XX Db 61 CTGATACCCCAAGCTGGGTGATCAGCGTGGCCACTGCTCTAGCAACAATACCAAGTT 120
XX
XX QY 50 HisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThrAlaThr 69

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Db      121 TGGCTGGGCGGAAACAACCTATTAGAGATGAACCATTTGCTCAGACCGGCTTGTCAGT 180
QY      70 GlusPheProHisProGlyPhe 77
Db      181 CAAAGCTTCCCTCACCCTGACTAC 204

RESULT 6
ABV33773/c
ID      ABV33773 standard; cDNA; 196 BP.
XX
AC      ABV33773;
XX
DT      16-SEP-2002 (first entry)
XX
DE      Human prostate expression marker cDNA 33764.
XX
KW      Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW      pharmacogenomic marker; gene; ss.
XX
OS      Homo sapiens.
XX
PN      WO200160860-A2.
XX
PD      23-AUG-2001.
XX
PF      20-FEB-2001; 2001WO-US005171.
XX
PR      17-FEB-2000; 2000US-0183319P.
PR      16-MAR-2000; 2000US-0189862P.
PR      25-MAY-2000; 2000US-0207454P.
PR      09-JUN-2000; 2000US-0211314P.
PR      18-JUL-2000; 2000US-0219007P.
PR      13-DEC-2000; 2000US-0225281P.
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI      Schlegel R, Endege WO, Monahan JE;
XX
WPI; 2001-662795/76.
XX
PT      Novel isolated nucleic acid molecule associated with cancerous state of
PT      prostate cells and correlating with presence of prostate cancer, useful
PT      for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS      Claim 1; Page 7129-7130; 11750pp; English.
XX
CC      The invention relates to an isolated nucleic acid molecule (I) comprising
CC      a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC      specification or its complement. (I) is useful for: (a) assessing whether
CC      a patient is afflicted with prostate cancer; (b) monitoring the
CC      progression of prostate cancer in a patient; (c) assessing the efficacy
CC      of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC      the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC      (e) selecting a composition for inhibiting prostate cancer in a patient;
CC      (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC      determining whether prostate cancer has metastasized in a patient; (h)
CC      assessing the aggressiveness or indolence of prostate cancer in a patient
CC      ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ      Sequence 196 BP; 53 A; 63 C; 47 G; 33 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          9.54e-07          Length:          196
Score:              169.00            Matches:         29
Percent Similarity: 80.00%            Conservative:     3
Best Local Similarity: 72.50%          Mismatches:      8
Query Match:        13.43%            Indels:          0
DB:                 5                  Gaps:            0

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US-09-856-320A-2_COPY_54_282 (1-229) x ABV33773 (1-196)
QY      173 GlyGlyLysAspSerCysGlnGlyProLeuValCysAsnGlnSerLeu 192

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Db      165 GGTGTAAAGACACTTGTGGGGGGATTCTGGGGGTGCACCTGTCTGTAATGGTGTGTT 106
QY      193 GlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyr 212
Db      105 CAAAGTATCACATCATGTGGGGCCCTGAGCCATGTGCCTGCCTGAAAGCCTGCTGTGTAC 46

RESULT 7
ABV42670/c
ID      ABV42670 standard; cDNA; 196 BP.
XX
AC      ABV42670;
XX
DT      16-SEP-2002 (first entry)
XX
DE      Human prostate expression marker cDNA 42661.
XX
KW      Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW      pharmacogenomic marker; gene; ss.
XX
OS      Homo sapiens.
XX
PN      WO200160860-A2.
XX
PD      23-AUG-2001.
XX
PF      20-FEB-2001; 2001WO-US005171.
XX
PR      17-FEB-2000; 2000US-0183319P.
PR      16-MAR-2000; 2000US-0189862P.
PR      25-MAY-2000; 2000US-0207454P.
PR      09-JUN-2000; 2000US-0211314P.
PR      18-JUL-2000; 2000US-0219007P.
PR      13-DEC-2000; 2000US-0225281P.
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI      Schlegel R, Endege WO, Monahan JE;
XX
WPI; 2001-662795/76.
XX
PT      Novel isolated nucleic acid molecule associated with cancerous state of
PT      prostate cells and correlating with presence of prostate cancer, useful
PT      for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS      Claim 1; Page 8534; 11750pp; English.
XX
CC      The invention relates to an isolated nucleic acid molecule (I) comprising
CC      a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC      specification or its complement. (I) is useful for: (a) assessing whether
CC      a patient is afflicted with prostate cancer; (b) monitoring the
CC      progression of prostate cancer in a patient; (c) assessing the efficacy
CC      of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC      the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC      (e) selecting a composition for inhibiting prostate cancer in a patient;
CC      (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC      determining whether prostate cancer has metastasized in a patient; (h)
CC      assessing the aggressiveness or indolence of prostate cancer in a patient
CC      ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ      Sequence 196 BP; 53 A; 63 C; 47 G; 33 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          9.54e-07          Length:          196
Score:              169.00            Matches:         29
Percent Similarity: 80.00%            Conservative:     3
Best Local Similarity: 72.50%          Mismatches:      8
Query Match:        13.43%            Indels:          0
DB:                 5                  Gaps:            0

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US-09-856-320A-2_COPY_54_282 (1-229) x ABV42670 (1-196)
QY      173 GlyGlyLysAspSerCysGlnGlyProLeuValCysAsnGlnSerLeu 192

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Db 165 GGTGTAAGACACTTGGGGGGGATCTGGGGGTCACCTGCTGTAATGGTGCCTT 106
Qy 193 GlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyr 212
Db 105 CAAGGTATCACATCATGCGCCCTGAGCCCAATGTCCTGCTGCTGCTGCTGCTGCTAC 46

RESULT 8
ID AAV60379 standard; mRNA; 200 BP.
XX AAV60379;
XX 07-DEC-1998 (first entry)
XX mRNA target sequence from exons 2 and 3 of PSA gene.
XX mRNA target sequence; prostate specific antigen; PSA; RNA purification;
XX ds.
XX Homo sapiens.
XX US5817798-A.
XX 06-OCT-1998.
XX 17-SEP-1997; 97US-00931981.
XX 17-SEP-1997; 97US-00931981.
XX (ABBO) ABBOTT LAB.
XX Gundling GJ;
XX WPI; 1998-556473/47.
XX Purification of RNA, used for nucleic acid amplification and disease
XX detection - by precipitating other sample components with transition
XX metal ions, separating and collecting the purified RNA.
XX Example 5; Col 9-10; 6pp; English.
XX The present sequence represents a mRNA target sequence from exons 2 and 3
XX of the prostate specific antigen (PSA) gene. The sequence is used to
XX exemplify the invention. The specification describes a method for
XX purifying RNA. The method comprises contacting a test sample with
XX polyvalent transition metal ions to form a precipitant and a supernatant,
XX separating the precipitant from the supernatant, and collecting the
XX supernatant to obtain a purified solution of total RNA. The RNA is used
XX for nucleic acid amplification and disease detection

XX SQ Sequence 200 BP; 31 A; 58 C; 67 G; 44 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.2e-06 Length: 200
Score: 168.00 Matches: 25
Percent Similarity: 74.55% Conservative: 16
Best Local Similarity: 45.45% Mismatches: 14
Query Match: 13.35% Indels: 0
DB: 2 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x AAV60379 (1-200)

Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20
Db 36 ATTGTGGAGCTGGGAGTGGAGAGCAATCCCAACCTGGCAGGTGCTTTGTGGCTCT 95
Qy 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
Db 96 CGTGGCAGGGAGGCTCGCGGGGNGTTCTGGTGACCCCGAGTGGGTCCTCACAGTGC 155
Qy 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsn 55

Db 156 CACTGCATCAGGAACAAAGCGTGATCTTGTGGTGGCAGCAGC 200
RESULT 9
ABK48905
ID ABK48905 standard; DNA; 154 BP.
XX ABK48905;
XX 02-JUL-2002 (first entry)
XX Novel human kallikrein KLK15, exon 2.
XX Kallikrein; KLK15; cancer; prostate cancer; colon cancer; kidney cancer;
XX testicular cancer; thyroid disorder; chromosome 19q13.3-q13.4; ds.
XX Homo sapiens.
XX WO200214485-A2.
XX 21-FEB-2002.
XX 10-AUG-2001; 2001WO-CAC01141.
XX 11-AUG-2000; 2000US-0224853P.
XX (MOUN) MOUNT SINAI HOSPITAL.
XX Yousef GM, Diamandis EP;
XX WPI; 2002-329575/36.
XX Novel kallikrein protein, KLK15 and nucleic acid molecule encoding the
XX protein useful for diagnosing, monitoring and treating thyroid disorders
XX and cancer, particularly prostate, colon, kidney and testicular cancer.
XX Claim 3; Page 61; 67pp; English.

XX The invention describes an isolated kallikrein protein (I) (KLK15) and
XX splice variants of (I). (I) is useful for identifying a substance which
XX associates with (I) and for evaluating a compound for its ability to
XX modulate the biological activity of (I). An anti-(I) antibody labeled
XX with a detectable substance is useful to detect KLK15 polypeptide in
XX biological samples, tissues and cells. The antibody is also useful for
XX monitoring the progression of cancer in an individual. (I) and the
XX polynucleotide encoding it are useful for treatment of a condition
XX mediated by KLK15 protein, in particular cancer (including prostate,
XX colon, kidney and testicular cancer) and thyroid disorders. This sequence
XX (located on chromosome 19q13.3-q13.4) represents exon 2 of the gene
XX encoding the novel human kallikrein protein (see ABK48346) described in
XX the invention
XX SQ Sequence 154 BP; 28 A; 51 C; 44 G; 31 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.98e-06 Length: 154
Score: 164.00 Matches: 26
Percent Similarity: 83.33% Conservative: 9
Best Local Similarity: 61.30% Mismatches: 7
Query Match: 13.04% Indels: 0
DB: 6 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x ABK48905 (1-154)

Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20
Db 21 TTGCTGGAGAGGTGACAGTGTGCACCCACCTCCAGCCATGGCAGTGGCTCTCTACAG 80
Qy 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
Db 81 CGTGGACCGCTTAACTGTGGGGCTTCCTCTCATCTCCACACATGGGTCTGTCTGGGCC 140
Qy 41 HisCys 42

Percent Similarity:	61.67%	Conservative:	10
Best Local Similarity:	45.00%	Mismatches:	23
Query Match:	13.04%	Indels:	0
DB:	6	Gaps:	0
US-09-856-320A-2_COPY_54_282 (1-229) x ABK30236 (1-216)			
QY	1	IleIleLysGlyPheGluCysLysProHisSerGlnProTrpClnAlaIateuPheGlu	20
DB	17	ATCATAAACGGCAGGAGTCTACGCCGCACTCGACGCCCTGGCAGCGGCTGTCATG	76
QY	21	LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla	40
DB	77	GAATAACGAATTTCTGCTCGGGCGTCTGGTGCATCCGACGTGGGTGCTGTNAGCGCA	136
QY	41	HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisasnLeuGluGlu	60
DB	137	CACGTGTTCCAGAACTCTACACACCTGGGCTGGGCTTNCACAGTTTNNAGCCGACCA	196
RESULT 11			
ID	ABN89908		
XX	ABN89908 standard; cDNA; 202 BP.		
XX	AC		
XX	ABN89908;		
DT	16-AUG-2002 (first entry)		
XX	Mouse clone DST IMX3_64 cDNA.		
DE	Mouse; antiinflammatory; gene therapy; ileitis; DST: ss; TOGA;		
KW	digital sequence tag; total gene expression analysis.		
XX			
OS	Mus musculus.		
XX			
PN	WO200231114-A2.		
XX			
PD	18-APR-2002.		
XX			
XX	11-OCT-2001; 2001WO-US032091.		
PF			
XX			
PR	11-OCT-2000; 2000US-0239483P.		
XX			
PA	(DIGI-) DIGITAL GENE TECHNOLOGIES INC.		
XX			
PI	Viney JL, Sims JE, Dubose RF, Baum PR, Hasel KW, Hilbush BS;		
XX			
DR	WPI; 2002-426279/45.		
XX			
PT	New isolated nucleic acid molecules that are associated with ileitis, for		
PT	preventing, treating, modulating and diagnosing ileitis in a mammalian		
PT	subject.		
XX			
PS	Claim 1; Page 184; 273pp; English.		
XX			
CC	The invention relates to a novel isolated nucleic acid molecule		
CC	comprising a polynucleotide having one of 90 polynucleotide sequences,		
CC	given in the specification. The polynucleotides of the invention have		
CC	antiinflammatory activity, and may have a use in gene therapy. The		
CC	polynucleotide or a polypeptide encoded by it is used for preventing,		
CC	treating, modulating or ameliorating a medical condition such as ileitis.		
CC	The polypeptide or polynucleotide is also useful for manufacturing a		
CC	medicament for treating ileitis. The sequence represents a cDNA digital		
CC	expression tag obtained from a mouse clone by the TOGA (total gene		
CC	expression analysis) method		
XX			
SQ	Sequence 202 BP; 55 A; 52 C; 45 G; 50 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	3,11e-06	Length:	202
Score:	163.50	Matches:	29
Percent Similarity:	74.47%	Conservative:	6
Best Local Similarity:	61.70%	Mismatches:	11
Query Match:	13.00%	Indels:	1

DB: 6 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x ABN89908 (1-202)

Qy 183 GlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleSerTrpGlyGlnAspPro 202
 Db 2 GGTAGCACTGTGGTCTGCAATAGAGAACTCCAGGGTATAGTCTCTCGGGGTATGGC--- 58
 Qy 203 CysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAspTrpIle 222
 Db 59 TGTGCGCTGCCAGACAATCCCTGGTGTGTACACCAAGGTCTGCAACTATGTGGACTGGATT 118
 Qy 223 GlnGluThrMetLysAsnAsn 229
 Db 119 CAGGACACAATGTGCGCCAC 139

RESULT 12
 ID AAT40842
 XX AAT40842 standard; cDNA; 207 BP.
 AC AAT40842;
 DT 15-MAR-1997 (first entry)
 XX Serine protease nFSP12 C-terminal fragment gene.
 DE XX
 XX Flea; midgut; serine protease; nFSP12; recombinant vaccine;
 KW domestic animal; infestation; insecticide; protease-inhibitor;
 KW controlled release formulation; synergist; ss.
 XX Siphonaptera sp.
 OS WO9611706-A1.
 XX PD 25-APR-1996.
 XX PF 18-OCT-1995; 95WO-US014442.
 XX PR 18-OCT-1994; 94US-00326773.
 PR 07-JUN-1995; 95US-00482130.
 PR 07-JUN-1995; 95US-00484211.
 PR 07-JUN-1995; 95US-00485443.
 PR 07-JUN-1995; 95US-00485455.
 XX (HESK-) HESKA CORP.
 XX Grieve RB, Rushlow KE, Hunter SW, Frank GR, Stiegler GL, Heath A;
 PI Yamanaka M, Arfsten A, Dale B;
 XX WPI; 1996-221762/22.
 DR P-PSDB; AAW01197.
 XX DNA encoding Flea serine protease and aminopeptidase - useful in vaccines
 PT to protect animals from flea infestation.
 XX Claim 70; Page 169; 24pp; English.
 CC This sequence encodes a C-terminal fragment of a flea midgut serine
 CC protease, nFSP12-225 (AAT40854), and has been isolated from a flea cDNA
 CC library by PCR using primers AAT40862-63 and hybridisation with probe
 CC AAT40866, based on conserved serine protease sequences. A corresponding N
 CC-terminal fragment, nFSP12-144 (AAT40836). The sequence may be used to
 CC produce a recombinant vaccine for protection of domestic animals from
 CC flea infestation, or in isolation of protease-inhibitors which may be
 CC used in controlled release formulations to reduce the flea burden on and
 CC around the animal. The inhibitors may be included in insecticidal
 CC compositions to increase efficacy of other active compounds, by reducing
 CC proteolytic activity in the flea midgut
 XX Sequence 207 BP; 55 A; 41 C; 47 G; 64 T; 0 U; 0 Other;
 SQ

Alignment Scores: 5.29e-05 Length: 207
 Pred. No.:

Score: 150.00 Matches: 32
 Percent Similarity: 72.73% Conservative: 8
 Best Local Similarity: 58.18% Mismatches: 13
 Query Match: 11.92% Indels: 3
 DB: 2 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x AAT40842 (1-207)

Qy 175 LysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly 194
 Db 43 AAGGTGCATGTAGGGGTATTCGGTGGCCCTTATCATCATCGACAACATTCATGGA 102
 Qy 195 IleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLys 214
 Db 103 ATTGTTTCTCTGGGCG---ATTCTTGGCTGT---CGCAAGCCTGATGTATTCAAGA 155
 Qy 215 ValCysLysTyrValAspTrpIleGlnGluThrMetLysAsnAsn 229
 Db 156 GTTTCATATTATGTCGATTGATTAAATCAAAATTTGAATAAAT 200

RESULT 13
 AAC90850
 ID AAC90850 standard; cDNA; 207 BP.
 XX AAC90850;
 AC AAC90850;
 DT 19-MAR-2001 (first entry)
 XX Flea serine protease nFSP12 N-terminal nucleotide sequence #76.
 DE XX
 XX Flea; cat flea; serine protease; aminopeptidase; cysteine protease;
 KW flea infestation; proteolytic; insecticide; vaccine; cat; dog; flea;
 KW Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;
 KW ectoparasite; ss.
 XX Ctenocephalides felis.
 OS US6150125-A.
 XX PD 21-NOV-2000.
 XX PF 24-APR-1996; 96US-00639075.
 XX PR 13-DEC-1991; 91US-00806482.
 PR 18-OCT-1994; 94US-00326773.
 PR 07-JUN-1995; 95US-00482130.
 PR 07-JUN-1995; 95US-00484211.
 PR 07-JUN-1995; 95US-00485443.
 PR 07-JUN-1995; 95US-00485455.
 PR 15-AUG-1997; 97WO-US014442.
 XX (HESK-) HESKA CORP.
 XX Gaines PJ, Silver G, Rushlow KE, Hunter SW, Frank GR;
 PI Stiegler GL, Grieve RB;
 XX WPI; 2001-136374/14.
 DR P-PSDB; AAB50594.
 XX New isolated flea proteins with proteolytic activity, useful for
 PT preventing and reducing flea infestations in mammals especially cats and
 PT dogs.
 XX Claim 4; Col 51-52; 150pp; English.
 PS The present invention describes isolated flea serine protease,
 XX aminopeptidase and cysteine protease proteins (I). Also described is a
 CC method for identifying a compound (II) capable of inhibiting flea
 CC protease activity comprising: (a) contacting (I) with a protease
 CC substrate and a putative inhibitory compound, where (I) has proteolytic
 CC activity in the absence of the compound; and (b) determining if the
 CC compound inhibits protease activity by detecting cleavage of the protease
 CC substrates; where decreased cleavage of the protease substrate indicates

CC an inhibitory compound. (I), nucleic acid molecules encoding (I), and
 CC antibodies immunospecific for (I) and (II) are useful for preventing and
 CC reducing flea infestations, particularly the species Ctenocephalides
 CC felis (cat fleas), Ctenocephalides canis (dog fleas) and Pulex irritans,
 CC in animals, preferably cats and dogs. They are also useful for reducing
 CC infestation by other ectoparasites, preferably mosquitoes, midges,
 CC sandflies, blackflies, ticks and Rhodnius. AAC90818 to AAC90913 and
 CC AAB50551 to AAB50644 represent sequences used in the exemplification of
 CC the present invention

XX Sequence 207 BP; 55 A; 41 C; 47 G; 64 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.29e-05 Length: 207
 Score: 150.00 Matches: 32
 Percent Similarity: 72.73% Conservative: 8
 Best Local Similarity: 58.18% Mismatches: 13
 Query Match: 11.92% Indels: 3
 DB: 4 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x AAC90850 (1-207)

QY 175 LysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly 194
 DB 43 AAGGGTCATGTAAGGGTGATTCGGGTGGCCCTTAGTCATCAATGACAACTTCATGGA 102
 QY 195 IleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLys 214
 DB 103 ATTGTTCTCCGGGGC---ATTCTCTGGCTGT---CGCAAGCCTGATGATTTCACAGA 155
 QY 215 ValCysLysTrpValAspTrpIleGlnGluThrMetLysAsnAsn 229
 DB 156 GTTCTCATATGTCGATTGGATTAAATCCAAATGTAATAAT 200

RESULT 14
 ABX46133
 ID ABX46133 standard; cDNA; 203 BP.

XX AC ABX46133;

XX 21-FEB-2003 (first entry)

XX Bovine EST associated with lactation/muscle/fat deposition #11299.

XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.

XX Bos Taurus.

XX US2002137139-A1.

XX 26-SEP-2002.

XX 24-SEP-2001; 2001US-00960352.

XX 12-JAN-1999; 99US-0115707P.

XX 11-JAN-2000; 2000US-00480902.

XX (BYATT/) BYATT J C.

XX (MATH/) MATHIALAGAN N.

XX (TAON/) TAO N.

XX (WARR/) WARREN W C.

XX Byatt JC, Mathialagan N, Tao N, Warren WC;

XX WPI; 2003-110599/10.

XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.

XX Claim 2; SEQ ID NO 11298; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX4836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non-translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 203 BP; 51 A; 55 C; 53 G; 44 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 5.72e-05 Length: 203
 Score: 149.50 Matches: 30
 Percent Similarity: 62.07% Conservative: 6
 Best Local Similarity: 51.72% Mismatches: 17
 Query Match: 11.88% Indels: 5
 DB: 7 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x ABX46133 (1-203)

QY 8 LysProHisSerGlnProTrpGlnAlaLeuPheGluLysThrArgLeuLeuCysGly 27
 DB 5 AAGCACACACTCTTGGCCCTGGCAAGTCAGCCTTCGAAGAAGCTCGAGGCACCTCTGTGGA 64

QY 28 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLys----- 44
 DB 65 GGAACCTGTGATATCCCAAGAGTGGTCTGACTGCTGCCCATTCCTGGACACATTTTA 124

QY 45 -----ProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
 DB 125 GCGCTGTCTATTCTACAAGGTCACTCTGGTGGCACACAAACGAAAGTCCGGGAA 178

RESULT 15

AAT92975
 ID AAT92975 standard; cDNA; 208 BP.

XX AC AAT92975;

XX 24-APR-1998 (first entry)

XX cDNA for prostate specific antigen (PSA).

XX Diagnosis; prostate cancer; prostate specific antigen; PSA;
 KW metastatic prostate cancer; prostate cell; secondary tumour;
 KW bone metastatic anchoring; ss.

XX Homo sapiens.

XX WO9739139-A1.

XX 23-OCT-1997.

XX 16-APR-1997; 97WO-US006497.

XX 16-APR-1996; 96US-0015765P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Robbins DJ;
 XX WPI; 1997-526473/48.
 XX Monitoring or diagnosis of prostate cancer - by detecting prostate-
 PT specific antigen mRNA using specific primers.
 XX Disclosure; Page 16; 25pp; English.
 XX cDNA sequences AAT92974-77 encode the prostate specific antigen (PSA).
 CC The detection of PSA mRNA in peripheral blood is associated with
 CC metastatic prostate cancer. Detection of PSA mRNA in the bloodstream
 CC indicates that prostate cells are circulating in the blood and confirms
 CC diagnosis of cancer. Circulating prostate cells also indicate a risk of a
 CC secondary tumour or bone metastatic anchoring. Detection of the PSA mRNA
 CC after prostatectomy or radiotherapy indicates a risk that the prostate
 CC cancer has spread and that the surgery and radiotherapy was not
 CC effective. PCR primers AAT92971-73 were used for the monitoring and
 CC diagnosis of patients with prostate cancer. The method comprises the
 CC detection of PSA mRNA by reverse transcriptase polymerase chain reaction
 CC (RT-PCR)
 XX
 XX Sequence 208 BP; 29 A; 62 C; 73 G; 44 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 9,928-05 Length: 208
 Score: 147.00 Matches: 22
 Percent Similarity: 75.00% Conservative: 11
 Best Local Similarity: 50.00% Mismatches: 11
 Query Match: 11.69% Indels: 0
 DB: 2 Gaps: 0
 US-09-856-320A-2_COPY_54_282 (1-229) x AAT92975 (1-208)
 QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
 DB 49 ATTGTGGAGGCTGGGAGTGGCAGAGCATTCACCAACCTGGCAGTGTGGCCCTCT 108
 QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
 DB 109 CGTGGCAGGCGCATGTGCGGCGGTTCGTGTCGACCCCGCAGTGGGTCTCACAGTCCC 168
 QY 41 HisCysLeuLys 44
 DB 169 CACTGCATCAGG 180
 RESULT 16
 AAT40854
 ID AAT40854 standard; cDNA; 225 BP.
 XX
 XX AAT40854;
 XX
 DT 16-MAR-1997 (first entry)
 XX
 DE Serine protease nFSP12-225 C-terminal fragment gene.
 XX
 KW Flea; midgut; serine protease; nFSP12-225; recombinant vaccine;
 KW domestic animal; infestation; insecticide; protease-inhibitor;
 KW controlled release formulation; synergist; ss.
 XX
 OS Siphonaptera sp.
 XX
 XX Key Location/Qualifiers
 FH 1..210
 FT CDS /*tag= b
 FT /*product= "Serine protease nFSP12-69 fragment"
 FT misc_feature 1..207
 FT /*tag= a

/note= "Sequence AAT40842 (claim 70)"
 FT
 XX WO9611706-A1.
 XX 25-APR-1996.
 XX 18-OCT-1995; 95WO-US014442.
 XX 18-OCT-1994; 94US-00326773.
 XX 07-JUN-1995; 95US-00482130.
 XX 07-JUN-1995; 95US-00484211.
 XX 07-JUN-1995; 95US-00485443.
 XX 07-JUN-1995; 95US-00485455.
 XX (HESK-) HESKA CORP.
 XX Grieve RB, Rushlow KE, Hunter SW, Frank GR, Stiegler GL, Heath A;
 XX Yamanaka M, Arfsten A, Dale B;
 XX WPI; 1996-221762/22.
 XX P-PSDE; AAT40854.
 XX DNA encoding Flea serine protease and aminopeptidase - useful in vaccines
 PT to protect animals from flea infestation.
 XX
 XX Claim 70; Page 187; 241pp; English.
 XX
 CC This sequence, nFSP12-225, encodes a C-terminal fragment of a flea midgut
 CC serine protease, PfSP12-69, and has been isolated from a flea cDNA
 CC library by PCR using primers AAT40862-63 and hybridisation with probe
 CC AAT40866, based on conserved serine protease sequences. The sequence
 CC contains a stop codon, and contains C-terminal sequence AAT40842. An N-
 CC terminal fragment of the protease gene, nFSP12-144 (AAT40836), has also
 CC been isolated. The sequence may be used to produce a recombinant vaccine
 CC for protection of domestic animals from flea infestation, or in isolation
 CC of protease-inhibitors which may be used in controlled release
 CC formulations to reduce the flea burden on and around the animal. The
 CC inhibitors may be included in insecticidal compositions to increase
 CC efficacy of other active compounds, by reducing proteolytic activity in
 CC the flea midgut
 XX
 XX Sequence 225 BP; 67 A; 43 C; 48 G; 67 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 0.00011 Length: 225
 Score: 147.00 Matches: 31
 Percent Similarity: 75.51% Conservative: 6
 Best Local Similarity: 63.27% Mismatches: 10
 Query Match: 11.69% Indels: 3
 DB: 2 Gaps: 2
 US-09-856-320A-2_COPY_54_282 (1-229) x AAT40854 (1-225)
 QY 175 LysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly 194
 DB 43 AAGGGTCATGTAAGGGTGATTCGGTGGCCCTTAGTCATCAATGGACAACTTCATGGA 102
 QY 195 IleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLys 214
 DB 103 ATTGTTTCTGGGGC---ATTCTTGGCTGT---CGCAAGCCTGATGATTCACAGA 155
 QY 215 ValCysLysTyrValAspTrpIleGln 223
 DB 156 GTTTTCATATTGTCGATTGGATTAA 182
 RESULT 17
 AAV04599
 ID AAV04599 standard; DNA; 225 BP.
 XX
 XX AAV04599;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-JUL-1998 (first entry)

XX DE Flea serine protease DNA sequence SEQ ID NO:131.
 XX KW Flea; Siphonaptera; protease; vaccine; prophylaxis; infestation;
 XX KW immunoglobulin protease; larvae; host animal; ss.

XX OS Siphonaptera.

XX PN WO9740058-A1:

XX PD 30-OCT-1997.

XX PF 24-APR-1997; 97WO-US006121.

XX PR 24-APR-1996; 96US-00639075.

XX PR 15-NOV-1996; 96US-00749699.

XX PR 04-APR-1997; 97US-0042945P.

XX PX (HESK-) HESKA CORP.

XX PI Grieve RB, Rushlow KE, Hunter SW, Frank GR, Steigler GL;

XX PI Gaines PJ, Silver G;

XX PX WPI; 1998-076762/07.

XX PT New flea protease genes and proteins - used in vaccine compositions for

XX PT the prophylaxis and treatment of flea infestation, especially in cats or

XX PT dogs.

XX PX Claim 1; Page 262; 318pp; English.

XX CC The present sequence is a DNA sequence from a novel flea serine protease.

XX CC The protease, its mimetopes, antibodies (Ab) and inhibitors of the

XX CC protein, as well as the DNA encoding the protein, may all be used in

XX CC therapeutic compositions to reduce flea protease activity (especially

XX CC immunoglobulin protease) and so reduce flea infestation, especially in

XX CC cats or dogs. Alternatively, flea larvae may ingest the faeces of adult

XX CC fleas which comprises anti-protease antibodies produced by a host animal

XX CC in response to administration of the protein. Therapeutic compositions

XX CC may further comprise a compound that reduces haematophagous ectoparasite

XX CC burden by a method other than by reducing flea immunoglobulin protease

XX CC activity. The novel flea DNA encoding the protein can also be used to

XX CC produce recombinant protein, and fragments of it are used as probes and

XX CC primers for identification and isolation of related sequences, also as

XX CC antisense, triplex-forming agents and ribozymes for inhibition of the

XX CC synthesis of the protein. Ab are also useful for screening expression

XX CC libraries, to purify the protein and to target cytotoxins to fleas.

XX CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 225 BP; 67 A; 43 C; 48 G; 67 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00011 Length: 225

Score: 147.00 Matches: 31

Percent Similarity: 75.51% Conservative: 6

Best Local Similarity: 63.27% Mismatches: 10

Query Match: 11.69% Indels: 3

DB: 2 Gaps: 2

RESULT 18

AAC90862

ID AAC90862 standard; cDNA; 225 BP.

XX AC AAC90862;

XX DT 19-MAR-2001 (first entry)

XX DE Flea serine protease nfSP12-225 nucleotide sequence #100.

XX KW Flea; cat flea; serine protease; aminopeptidase; cysteine protease;

XX KW flea infestation; proteolytic; insecticide; vaccine; cat; dog; flea;

XX KW Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;

XX KW ectoparasite; ss.

XX OS Ctenocephalides felis.

XX PX US6150125-A.

XX PD 21-NOV-2000.

XX PF 24-APR-1996; 96US-00639075.

XX PR 13-DEC-1991; 91US-00806482.

XX PR 18-OCT-1994; 94US-00326773.

XX PR 07-JUN-1995; 95US-00482130.

XX PR 07-JUN-1995; 95US-00484211.

XX PR 07-JUN-1995; 95US-00485443.

XX PR 07-JUN-1995; 95US-00485455.

XX PR 15-AUG-1997; 97WO-US014442.

XX PX (HESK-) HESKA CORP.

XX PI Gaines PJ, Silver G, Rushlow KE, Hunter SW, Frank GR;

XX PI Stiegler GL, Grieve RB;

XX PX WPI; 2001-136374/14.

XX PR P-PSDB; AAB50606.

XX PT New isolated flea proteins with proteolytic activity, useful for

XX PT preventing and reducing flea infestations in mammals especially cats and

XX PT dogs.

XX PX Claim 4; Col 161-162; 150pp; English.

XX CC The present invention describes isolated flea serine protease,

XX CC aminopeptidase and cysteine protease proteins (I). Also described is a

XX CC method for identifying a compound (II) capable of inhibiting flea

XX CC protease activity comprising: (a) contacting (I) with a protease

XX CC substrate and a putative inhibitory compound, where (I) has proteolytic

XX CC activity in the absence of the compound; and (b) determining if the

XX CC compound inhibits protease activity by detecting cleavage of the protease

XX CC substrates; where decreased cleavage of the protease substrate indicates

XX CC an inhibitory compound. (I), nucleic acid molecules encoding (I), and

XX CC antibodies immunospecific for (I) and (II) are useful for preventing and

XX CC reducing flea infestations, particularly the species Ctenocephalides

XX CC felis (cat fleas), Ctenocephalides canis (dog fleas) and Pulex irritans,

XX CC in animals, preferably cats and dogs. They are also useful for reducing

XX CC infestation by other ectoparasites, preferably mosquitoes, midges,

XX CC sandflies, blackflies, ticks and Rhodnius. AAC90818 to AAC90913 and

XX CC AAB50551 to AAB50644 represent sequences used in the exemplification of

XX CC the present invention

SQ Sequence 225 BP; 67 A; 43 C; 48 G; 67 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00011 Length: 225

Score: 147.00 Matches: 31

Percent Similarity: 75.51% Conservative: 6

Best Local Similarity: 63.27% Mismatches: 10

Query Match: 11.69% Indels: 3

DB: 4 Gaps: 2

QY 175 LysAspSerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGly 194

Db 43 AAGGGTGCATGTAAGGCGTATCCGGTGGCCCTTAGTCATCAATGCACTTCATGGA 102

QY 195 IleIleSerTrpGlnAspProCysAlaIleThrArgGlyProGlyValTrpThrLys 214

Db 103 ATGTGTTCTCCGGGGC---ATTCTTCGGCTGT---CGCAAGCCTGATGATATCAAGA 155

QY 215 ValCysLysTrpValAspTrpIleGln 223

Db 156 GTTCTTCATATGTCGATTGATTAA 182

US-09-856-320A-2_COPY_54_282 (1-229) x AAC90862 (1-225)

QY 175 LysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly 194
Db 43 AAGGTGATGATGAGGGGATTCGGTGGCCCTTAGTCATCAATGACAACTTCATGGA 102
QY 195 IleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTrpThyls 214
Db 103 ATTGTTCTCTGGGC---ATTCTTCTGGCTGT---CGCAAGCCTGATGATTACACAAGA 155
QY 215 ValCysLysTyrValAspTrpIleGln 223
Db 156 GTTCTCATTATGTCGATTGGATTAAA 182

RESULT 19
AAT40847
ID AAT40847 standard; cDNA; 218 BP.
XX AAT40847;
AC AAT40847;
DT 16-MAR-1997 (first entry)
XX Serine protease nfSP5-218 gene.
DE Flea; midgut; serine protease; nfSP5-218; recombinant vaccine;
KW domestic animal; infestation; insecticide; protease-inhibitor;
KW controlled release formulation; synergist; ss.
XX Siphonaptera sp.

Key Location/Qualifiers
CDS 3..218
FT /tag= a
FT /product= "serine protease PfSP5-72"
FT misc_feature 42..203
FT /tag= b
FT /note= "nfSP5-159 (AAT40823, claim 70)"

PN WO9611706-A1.
XX 25-APR-1996.
XX 18-OCT-1995; 95WO-US014442.
XX 18-OCT-1994; 94US-00326773.
XX 07-JUN-1995; 95US-00482130.
XX 07-JUN-1995; 95US-00484211.
XX 07-JUN-1995; 95US-00485443.
XX 07-JUN-1995; 95US-00485455.
XX (HESK-) HESKA CORP.
XX Grieve RB, Rushlow KE, Hunter SW, Frank GR, Stiegler GL, Heath A;
PI Yamanaka M, Arfsten A, Dale B;
XX WPI; 1996-221762/22.
DR P-PSDB; AAW01202.
XX DNA encoding Flea serine protease and aminopeptidase - useful in vaccines
PI to protect animals from flea infestation.
XX Claim 70; Page 176; 241pp; English.

XX This sequence (nfSP5-218) encodes a flea midgut serine protease partial
CC sequence (PfSP5-72), and has been isolated from a flea cDNA library by
CC PCR using primers AAT40862-63 and hybridisation with probe AAT40866,
CC based on conserved serine protease sequences. The sequence contains
CC sequence AAT40823 (nfSP5-159), which spans 2 conserved serine protease
CC sequences, and an additional partial sequence is given in AAT40846 (nfSP5
CC -157). The sequence may be used to produce a recombinant vaccine for
CC protection of domestic animals from flea infestation, or in isolation of
CC protease-inhibitors which may be used in controlled release formulations
CC to reduce the flea burden on and around the animal. The inhibitors may be

CC included in insecticidal compositions to increase efficacy of other
CC active compounds, by reducing proteolytic activity in the flea midgut
SQ Sequence 218 BP; 60 A; 48 C; 52 G; 58 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00013 Length: 218
Score: 146.00 Matches: 30
Conservative: 13
Percent Similarity: 59.72% Mismatches: 23
Best Local Similarity: 41.67% Indels: 6
Query Match: 11.61% Gaps: 3
DB: 2

US-09-856-320A-2_COPY_54_282 (1-229) x AAT40847 (1-218)

QY 115 ValThrAlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSer-----Pro 132
Db 12 TTAACACCTGGAACATATGTGCACTGTACTGGATGGGATCAACTGGATCTGGTGCTCA 71
QY 133 GlnLeuArgLeuProHisThrIleuArgCysAlaAsnIleThrIleIleGluHisGlnLys 152
Db 72 -----ATTACAAATGTTCTACAAAGTTCGAAGTTCATTTATCGACTTCAACACC 122
QY 153 CysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSer---ValGln 171
Db 123 TGGCGAAATCCTACTCAACACGCTTAACGACCGATGTTCTGGCGCTGGATTTTGGGA 182
QY 172 GluGlyGlyLysAspSerCysGlnGlyAspSerGly 183
Db 183 ATTGTTGTTAAGACCGCTTGCACGACGACTCCGGA 218

RESULT 20
RAV04590
ID AAV04590 standard; DNA; 218 BP.

XX AAV04590;
AC AAV04590;
DT 25-MAR-2003 (revised)
DT 02-JUL-1998 (first entry)
XX Flea serine protease DNA sequence SEQ ID NO:117.
DE Flea; Siphonaptera; protease; vaccine; prophylaxis; infestation;
KW immunoglobulin protease; larvae; host animal; ss.
XX Siphonaptera.

XX WO9740058-A1.
XX 30-OCT-1997.
XX 24-APR-1997; 97WO-US006121.
XX 24-APR-1996; 96US-00639075.
XX 15-NOV-1996; 96US-00749699.
XX 04-APR-1997; 97US-0042945P.
XX (HESK-) HESKA CORP.
XX Grieve RB, Rushlow KE, Hunter SW, Frank GR, Steigler GL;
PI Gaines PJ, Silver G;
XX WPI; 1998-076762/07.
XX New flea protease genes and proteins - used in vaccine compositions for
PT the prophylaxis and treatment of flea infestation, especially in cats or
PT dogs.

XX Claim 1; Page 253; 318pp; English.
XX The present sequence is a DNA sequence from a novel flea serine protease.
CC The protease, its mimetopes, antibodies (Ab) and inhibitors of the
CC protein, as well as the DNA encoding the protein, may all be used in

therapeutic compositions to reduce flea protease activity (especially immunoglobulin protease) and so reduce flea infestation, especially in cats or dogs. Alternatively, flea larvae may ingest the faeces of adult fleas which comprises anti-protease antibodies produced by a host animal in response to administration of the protein. Therapeutic compositions may further comprise a compound that reduces haematophagous ectoparasite burden by a method other than by reducing flea immunoglobulin protease activity. The novel flea DNA encoding the protein can also be used to produce recombinant protein, and fragments of it are used as probes and primers for identification and isolation of related sequences, also as antisense, triplex-forming agents and ribozymes for inhibition of the synthesis of the protein. Ab are also useful for screening expression libraries, to purify the protein and to target cytotoxins to fleas.

(Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 218 BP; 60 A; 48 C; 52 G; 58 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00013 Length: 218
Score: 146.00 Matches: 30
Percent Similarity: 59.72% Conservative: 13
Best Local Similarity: 41.67% Mismatches: 23
Query Match: 11.61% Indels: 6
DB: 2 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x AAV04590 (1-218)

QY 115 ValThrAlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSer-----Pro 132
Db 12 TTAACACCTGGAACTATGTGCACTGTTACTGATGGGATCAACTGATCGTGGTCCA 71
QY 133 GlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleIleGluHisGlnLys 152
Db 72 -----ATTCAAAATGTTCTACAGAACTGCAAGTTCATTTATCGACTTCAACACC 122
QY 153 CysGluAsnAlaTyPrOGlyAsnIleThrAspThrMetValCysAlaSer---ValGln 171
Db 123 TGCAGAAATCCTACTACACAGCTTACACGACCGTATGTTCTGCGCTGGATTTTGGGA 182
QY 172 GluGlyGlyLysAspSerCysGlnGlyAspSerGly 183
Db 183 ATTGGTGGTAAAGACGCTTCCCAAGGCGACTCCGGA 218

RESULT 21

AAC90855
ID AAC90855 standard; cDNA; 218 BP.

XX AAC90855;

AC AAC90855;

DT 19-MAR-2001 (first entry)

DE Flea serine protease nFSP5-218 nucleotide sequence #86.

XX Flea, cat flea; serine protease; aminopeptidase; cysteine protease;
KW flea infestation; proteolytic; insecticide; vaccine; cat; dog; flea;
KW Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;
KW ectoparasite; ss.

OS Ctenocephalides felis.

XX US6150125-A.

PN 21-NOV-2000.

XX 24-APR-1996; 96US-00639075.

XX 13-DEC-1991; 91US-00806482.

PR 18-OCT-1994; 94US-00328773.

PR 07-JUN-1995; 95US-00482130.

PR 07-JUN-1995; 95US-00484211.

PR 07-JUN-1995; 95US-00485443.

PR 07-JUN-1995; 95US-00485455.

PR 15-AUG-1997; 97NO-US014442.

XX (HESK-) HESKA CORP.
PA Gaines PJ, Silver G, Rushlow KE, Hunter SW, Frank GR;
XX Stiegler GL, Grieve RB;
PI WPI; 2001-136374/14.
XX P-PSDB; AAB50599.
DR New isolated flea proteins with proteolytic activity, useful for
XX preventing and reducing flea infestations in mammals especially cats and
XX dogs.
PS Claim 4; Col 143-144; 150pp; English.

XX The present invention describes isolated flea serine protease,
CC aminopeptidase and cysteine protease proteins (I). Also described is a
CC method for identifying a compound (II) capable of inhibiting flea
CC protease activity comprising: (a) contacting (I) with a protease
CC substrate and a putative inhibitory compound, where (I) has proteolytic
CC activity in the absence of the compound; and (b) determining if the
CC compound inhibits protease activity by detecting cleavage of the protease
CC substrates, where decreased cleavage of the protease substrate indicates
CC an inhibitory compound. (I), nucleic acid molecules encoding (I), and
CC antibodies immunospecific for (I) and (II) are useful for preventing and
CC reducing flea infestations, particularly the species Ctenocephalides
CC felis (cat fleas), Ctenocephalides canis (dog fleas) and Pulex irritans,
CC in animals, preferably cats and dogs. They are also useful for reducing
CC infestation by other ectoparasites, preferably mosquitoes, midges,
CC sandflies, blackflies, ticks and Rhodnius. AAC90818 to AAC90913 and
CC AAB50551 to AAB50644 represent sequences used in the exemplification of
CC the present invention

XX Sequence 218 BP; 60 A; 48 C; 52 G; 58 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00013 Length: 218
Score: 146.00 Matches: 30
Percent Similarity: 59.72% Conservative: 13
Best Local Similarity: 41.67% Mismatches: 23
Query Match: 11.61% Indels: 6
DB: 2 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x AAC90855 (1-218)

QY 115 ValThrAlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSer-----Pro 132
Db 12 TTAACACCTGGAACTATGTGCACTGTTACTGATGGGATCAACTGATCGTGGTCCA 71
QY 133 GlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleIleGluHisGlnLys 152
Db 72 -----ATTCAAAATGTTCTACAGAACTGCAAGTTCATTTATCGACTTCAACACC 122
QY 153 CysGluAsnAlaTyPrOGlyAsnIleThrAspThrMetValCysAlaSer---ValGln 171
Db 123 TGCAGAAATCCTACTACACAGCTTACACGACCGTATGTTCTGCGCTGGATTTTGGGA 182
QY 172 GluGlyGlyLysAspSerCysGlnGlyAspSerGly 183
Db 183 ATTGGTGGTAAAGACGCTTCCCAAGGCGACTCCGGA 218

RESULT 22

ABK48911
ID ABK48911 standard; DNA; 137 BP.

XX AC ABK48911;

DT 02-JUL-2002 (first entry)

DE Novel human kallikrein KLK15, exon 4.

XX Kallikrein; KLK15; cancer; prostate cancer; colon cancer; kidney cancer;
KW testicular cancer; thyroid disorder; chromosome 19q13.3-q13.4; ds.

OS	Homo sapiens.	XX	WO2000192581-A2.	XX	06-DEC-2001.	XX	29-MAY-2001; 2001WO-US017756.	XX	26-MAY-2000; 2000US-0207484P.	XX	(CORI-) CORIXA CORP.	XX	Algate PA, Harlocker SL, Jones R;	XX	WPI; 2002-122075/16.	XX	Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of an ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.	XX	Claim 1; SEQ ID NO 3234; 489pp; English.	XX	The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of an ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contracting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques	XX	Sequence 163 BP; 36 A; 40 C; 51 G; 36 T; 0 U; 0 Other;	SQ	Alignment Scores:	Pred. No.:	0.000714	Length:	163	Score:	136.00	Matches:	25	Percent Similarity:	64.81%	Conservative:	10	Best Local Similarity:	46.30%	Mismatches:	19	Query Match:	10.81%	Indels:	0	Gaps:	0	DB:	US-09-856-320A-2_COPY_54_282 (1-229) x ABL80256 (1-163)	Qy	176 AspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 195	Db	163 AACTCTCCCAAGGGGAATTCCTGGGGCCCTTTGGTCCCTCAATGGCTCTCGCAGGAGCC 104	Qy	196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTrpThrLysVal 215	Db	103 GTGTCTGGGGATATTACCTTTGTGCGCGGCCCAACAGACCGGTTTCTTACAGCACTC 44	Qy	216 CysLysTrpValAspTrpIleGlnGluThrMetLysAsnAsn 229	Db	43 TGCAAGTTTCCCAAGTGGATCCAGGAACCATCCAGGCCAAC 2	RESULT 24	AAQ31930	ID	AAQ31930 standard; DNA; 205 BP.	XX	AAQ31930;	AC	AAQ31930;										
XX	Homo sapiens.	XX	WO200214485-A2.	XX	21-FEB-2002.	XX	10-AUG-2001; 2001WO-CA001141.	XX	11-AUG-2000; 2000US-0224853P.	XX	(MOUN) MOUNT SINAI HOSPITAL.	XX	Yousef GM, Diamandis EP;	XX	WPI; 2002-329575/36.	XX	Novel kallikrein protein, KLK15 and nucleic acid molecule encoding the protein useful for diagnosing, monitoring and treating thyroid disorders and cancer, particularly prostate, colon, kidney and testicular cancer.	XX	Claim 3; Page 62; 67pp; English.	XX	The invention describes an isolated kallikrein protein (I) (KLK15) and splice variants of (I). (I) is useful for identifying a substance which associates with (I) and for evaluating a compound for its ability to modulate the biological activity of (I). An anti-(I) antibody labelled with a detectable substance is useful to detect KLK15 polypeptide in biological samples, tissues and cells. The antibody is also useful for monitoring the progression of cancer in an individual. (I) and the polynucleotide encoding it are useful for treatment of a condition mediated by KLK15 protein, in particular cancer (including prostate, colon, kidney and testicular cancer) and thyroid disorders. This sequence (located on chromosome 19q13.3-q13.4) represents exon 4 of the gene encoding the novel human kallikrein protein (see ABK48346) described in the invention	XX	Sequence 137 BP; 34 A; 36 C; 40 G; 27 T; 0 U; 0 Other;	SQ	Alignment Scores:	Pred. No.:	0.000572	Length:	137	Score:	136.00	Matches:	23	Percent Similarity:	70.45%	Conservative:	8	Best Local Similarity:	52.27%	Mismatches:	13	Query Match:	10.81%	Indels:	0	Gaps:	0	DB: <td>US-09-856-320A-2_COPY_54_282 (1-229) x ABK48911 (1-137)</td> <td>Qy</td> <td>136 LeuProHisThrIleuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsn 155</td> <td>Db</td> <td>6 CTCCAGATACGTTGATGTTGTCACATCATCATCATCATCATCATCATCATCATCATCAT 65</td> <td>Qy</td> <td>156 AlaTrpProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLys 175</td> <td>Db</td> <td>66 AGTACCCAGGGCGCTGACAAACACCATGTTGTGAGGCGCGGAGGAGGAGGAGGAGG 125</td> <td>Qy</td> <td>176 AspSerCysGln 179</td> <td>Db</td> <td>126 GAATCTGTGAG 137</td> <td>RESULT 23</td> <td>ABL80256/c</td> <td>ID</td> <td>ABL80256 standard; cDNA; 163 BP.</td> <td>XX</td> <td>ABL80256;</td> <td>AC</td> <td>ABL80256;</td> <td>XX</td> <td>17-MAY-2002 (first entry)</td> <td>XX</td> <td>Human ovarian cancer related cDNA clone SEQ ID NO:3234.</td> <td>DE</td> <td>Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.</td> <td>XX</td> <td></td> <td>XX</td> <td></td>	US-09-856-320A-2_COPY_54_282 (1-229) x ABK48911 (1-137)	Qy	136 LeuProHisThrIleuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsn 155	Db	6 CTCCAGATACGTTGATGTTGTCACATCATCATCATCATCATCATCATCATCATCATCAT 65	Qy	156 AlaTrpProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLys 175	Db	66 AGTACCCAGGGCGCTGACAAACACCATGTTGTGAGGCGCGGAGGAGGAGGAGGAGG 125	Qy	176 AspSerCysGln 179	Db	126 GAATCTGTGAG 137	RESULT 23	ABL80256/c	ID	ABL80256 standard; cDNA; 163 BP.	XX	ABL80256;	AC	ABL80256;	XX	17-MAY-2002 (first entry)	XX	Human ovarian cancer related cDNA clone SEQ ID NO:3234.	DE	Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.	XX		XX	

XX DT 18-JAN-1993 (first entry)
 XX DE Human scu-PA54 gene fragment M6 (O14-O16; O14A-O16A,B).
 XX KW Single chain urokinase-type plasminogen activator; expression; plasmid;
 XX KW ds.
 XX OS Synthetic.
 XX PN DR4101736-A.
 XX PD 23-JUL-1992.
 XX PF 22-JAN-1991; 91DE-04101736.
 XX PR 22-JAN-1991; 91DE-04101736.
 XX PA (CHEF) GRUENENTHAL GMBH.
 XX PI Steffens GJ, Guenzler WA, Flohe L, Brigelius-Flohe RE, Wolf B;
 XX DR WPI; 1992-251111/31.
 XX PT New recombinant peptide(s) contg. non-glycosylated scu-PA 54k sequence -
 XX PT used as plasminogen activators, for treatment of infarction and to
 XX PT prevent accumulation of platelets on thrombogenic surfaces.
 XX PS Disclosure; Fig 6(c); 32pp; German.
 XX CC The 3'- and 5'-end of the antisense strand overhangs the sense strand by
 XX CC 4 bases. Synthetic fragments M4-M8 (AAQ25893 and AAQ31929-32) are used in
 XX CC the prodn. of the scu-PA gene. The gene was used in plasmids for
 XX CC expression of recombinant scu-PA43k (see AAR25395-404) in
 XX CC Enterobacteriaceae (esp. E.coli). The plasmids also contain an operon
 XX CC consisting of a regulatable promoter (see AAQ31933); a Shine-Dalgarno
 XX CC sequence effective as ribosome-binding site; a start codon and 1 or 2
 XX CC terminators
 XX SQ Sequence 205 BP; 54 A; 59 C; 46 G; 46 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.00118 Length: 205
 Score: 135.00 Matches: 26
 Percent Similarity: 58.82% Conservative: 14
 Best Local Similarity: 38.24% Mismatches: 26
 Query Match: 10.73% Indels: 2
 DB: 2 Gaps: 1
 US-09-856-320A-2_COPY_54_282 (1-229) x AAQ31930 (1-205)
 QY 120 SerCysLeuSerGlyThrPglYSerThrSerProGlnLeuArgLeuProHisThr 139
 Db 2 TCTTGGAAATCACCCTGTTTCGGTAAAGAAACTCTACCGACTACCTGTACCGGAACAG 61
 QY 140 LeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGlu-----AsnAlaTyr 157
 Db 62 CTGAATGATGACCGTTGTAAACTGATCTCTCCCGTGAATGCGCAGCGGCACACTACTAC 121
 QY 158 ProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSer 177
 Db 122 GGTTCTGAAGTACCACCAAAATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 QY 178 CysGlnGlyAspSerGlyGlyPro 185
 Db 182 TGCCAAAGGTGACTCTGTGTGTCCA 205
 RESULT 25
 AAX57985
 ID AAX57985 standard; DNA; 227 BP.
 XX AC AAX57985;
 XX

DT 19-JUL-1999 (first entry)
 XX DE Human BS247 specific polynucleotide #3.
 XX KW BS247; detection; diagnosis; breast cancer; atypical hyperplasia;
 XX KW fibroadenoma; cystic breast disease; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN WO9922027-A1.
 XX PD 06-MAY-1999.
 XX PF 28-OCT-1998; 98WO-US022906.
 XX PR 28-OCT-1997; 97US-0063431P.
 XX PR 28-OCT-1997; 97US-00968838.
 XX PA (ABBO) ABBOTT LAB.
 XX PI Billings-Medel PA, Cohen W, Colpitts TL, Friedman PN, Gordon J;
 XX PI Granados EN, Hodges SC, Klass MK, Kratochvil JD, Russell JC;
 XX PI Stroupe SD, Yu H;
 XX DR WPI; 1999-312977/26.
 XX PT Breast tissue derived cDNA contig and consensus polypeptide sequence.
 XX PS Claim 1; Page 104; 112pp; English.
 XX CC This sequence is a BS247 specific polynucleotide. The invention relates
 XX CC to a method of detecting the presence of a target BS247 polynucleotide,
 XX CC especially mRNA, in a test sample. BS247 polynucleotides are derived from
 XX CC breast tissue. The polynucleotides, polypeptides or antibodies are useful
 XX CC for providing information leading to the detection, diagnosis, staging,
 XX CC monitoring, prognosis, in vivo imaging, prevention or treatment,
 XX CC determining predisposition to, diseases and conditions of the breast,
 XX CC such as breast cancer, atypical hyperplasia, fibroadenoma and cystic
 XX CC breast disease. Drug treatment or gene therapy for breast cancer, can be
 XX CC based on these identified gene sequences and the efficacy of any
 XX CC particular therapy can be monitored. The BS247-derived reagents are
 XX CC advantageous for detection of breast cancer due to their specificity. The
 XX CC reagents also provide an alternative, non-surgical diagnostic method
 XX CC capable of detecting early stage breast disease, such as cancer
 XX SQ Sequence 227 BP; 55 A; 80 C; 42 G; 50 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.00149 Length: 227
 Score: 134.50 Matches: 30
 Percent Similarity: 56.41% Conservative: 14
 Best Local Similarity: 38.46% Mismatches: 29
 Query Match: 10.69% Indels: 5
 DB: 2 Gaps: 2
 US-09-856-320A-2_COPY_54_282 (1-229) x AAX57985 (1-227)
 QY 38 ThrAlaAlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGln 57
 Db 2 ACGGCGCCCACTCGAGAGAAAGTTTTCAGAGTCTCGTCTCGGCCACTACTCCCTGTCA 61
 QY 58 Lys---GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGly 76
 Db 62 CCAGTTTATGAATCTGGCGAGAGATGTTCCAGGGGTCAATCCATCCCCACCTGGC 121
 QY 77 PheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAla 96
 Db 122 TACTCC-----CACCCTGGCCACTCTTAACGACCTCATGCTCATCAAACTGAAC 169
 QY 97 SerProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCys 114
 Db 170 AGAAGAATTCTGCCACTAAAGATGTCAGACCCATCAACGTCCTCTCTATTGT 223

RESULT 26

AAZ89009
ID AAZ89009 standard; DNA; 180 BP.
XX
AC AAZ89009;
XX
DT 02-JUN-2000 (first entry)
XX
XX
DE Rat Factor IX DNA fragment.
XX
KW RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;
KW RNA amplification with transcript sequencing; rat; ss.
XX
OS Rattus sp.
XX
XX
PN US6027913-A.
XX
XX
PD 22-FEB-2000.
XX
XX
PF 27-DEC-1994; 94US-00399855.
XX
XX
PR 28-JAN-1988; 88US-00149312.
PR 24-JUL-1989; 89US-00385013.
PR 12-NOV-1993; 93US-00151461.
XX
XX
PA (SOMM/) SOMMER S S.
XX
XX
PI Sommer SS;
XX
XX
DR WPI; 2000-194830/17.
DR P-PSDB; AAY51619.
XX
XX
PT Producing polypeptides from nucleic acid sequences of interest using a
PT modified RAWIT (RNA amplification with in vitro translation) method.
XX
XX
PS Disclosure; Fig 4; 65pp; English.
XX
XX
CC This invention describes a novel modified RAWIT (RNA amplification with
CC in vitro translation) method, for synthesizing polypeptides encoded by
CC sequences of interest. The method generates a protein from an RNA
CC molecule and comprises (a) incubating the RNA with reverse transcriptase
CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies
CC of the cDNA in the presence of at least 1 oligonucleotide primer which
CC contains an RNA promoter sequence; (c) transcribing the DNA generated
CC with an RNA polymerase to form RNA transcripts; and (d) translating the
CC RNA transcripts in vitro to generate the protein. This sequence encodes a
CC fragment of the rat Factor IX protein which is used to illustrate the
CC RAWTS (RNA amplification with transcript sequencing) method of the
CC invention
XX
SQ Sequence 180 BP; 62 A; 30 C; 41 G; 47 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00186 Length: 180
Score: 132.00 Matches: 24
Percent Similarity: 58.33% Conservative: 11
Best Local Similarity: 40.00% Mismatches: 23
Query Match: 10.49% Indels: 2
DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89009 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
DB 1 AAAGTTGATGCATCTCTGTGAGCGGCATCATTAATGAATAATGGAATGTAATGCTGCC 60
QY 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 58
DB 61 CACTGTCTTAACCTGGTGATAAAATGAGTTGTTGCTGGTGAACATAATATGATGAG 120
QY 59 GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78
DB 121 AAGGAAGACAGACAGAAAGAGAAATGTGATTGGAACATATCCCTCATCACCAGTACAAT 180

RESULT 27

AAZ89011
ID AAZ89011 standard; DNA; 180 BP.
XX
AC AAZ89011;
XX
DT 02-JUN-2000 (first entry)
XX
XX
DE Rabbit Factor IX DNA fragment.
XX
KW RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;
KW RNA amplification with transcript sequencing; rabbit; ss.
XX
XX
OS Oryctolagus cuniculus.
XX
XX
PN US6027913-A.
XX
XX
PD 22-FEB-2000.
XX
XX
PF 27-DEC-1994; 94US-00399855.
XX
XX
PR 28-JAN-1988; 88US-00149312.
PR 24-JUL-1989; 89US-00385013.
PR 12-NOV-1993; 93US-00151461.
XX
XX
PA (SOMM/) SOMMER S S.
XX
XX
PI Sommer SS;
XX
XX
DR WPI; 2000-194830/17.
DR P-PSDB; AAY51620.
XX
XX
PT Producing polypeptides from nucleic acid sequences of interest using a
PT modified RAWIT (RNA amplification with in vitro translation) method.
XX
XX
PS Disclosure; Fig 4; 65pp; English.
XX
XX
CC This invention describes a novel modified RAWIT (RNA amplification with
CC in vitro translation) method, for synthesizing polypeptides encoded by
CC sequences of interest. The method generates a protein from an RNA
CC molecule and comprises (a) incubating the RNA with reverse transcriptase
CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies
CC of the cDNA in the presence of at least 1 oligonucleotide primer which
CC contains an RNA promoter sequence; (c) transcribing the DNA generated
CC with an RNA polymerase to form RNA transcripts; and (d) translating the
CC RNA transcripts in vitro to generate the protein. This sequence encodes a
CC fragment of the rabbit Factor IX protein which is used to illustrate the
CC RAWTS (RNA amplification with transcript sequencing) method of the
CC invention
XX
SQ Sequence 180 BP; 55 A; 37 C; 41 G; 47 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00229 Length: 180
Score: 131.00 Matches: 22
Percent Similarity: 63.64% Conservative: 13
Best Local Similarity: 40.00% Mismatches: 18
Query Match: 10.41% Indels: 2
DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89011 (1-180)

QY 26 CysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysPro 45
DB 16 TGTGAGGTTCCATCGTTGTAATGAATAATGGTTGTAATGAGCCCTGCATCAGCCT 75
QY 46 -----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGlu 63
DB 76 GGTGTAAATTAATTACTGTGTTGTCAGGTGACATACATGAGAGCCAGACCTACAGAG 135
QY 64 GlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78

Db 136 CAAAAGCGAATGTGATCCGTGCTATTCTTACCACGTTACAAT 180

RESULT 28

AAZ89008

ID AAZ89008 standard; DNA; 180 BP.

XX AAZ89008;

AC AAZ89008;

DT 02-JUN-2000 (first entry)

DE Murine Factor IX DNA fragment.

DE RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;

KW RNA amplification with transcript sequencing; mouse; ss.

XX Mus sp.

OS US6027913-A.

XX 22-FEB-2000.

PD 27-DEC-1994; 94US-00399855.

PF 28-JAN-1988; 88US-00149312.

PR 24-JUL-1989; 89US-00385013.

PR 12-NOV-1993; 93US-00151461.

XX (SOMM/) SOMMER S S.

FA Sommer SS;

XX WPI; 2000-194830/17.

XX P-PSDB; AAY51618.

DR Producing polypeptides from nucleic acid sequences of interest using a

PT modified RAWIT (RNA amplification with in vitro translation) method.

XX Disclosure; Fig 4; 65pp; English.

PS This invention describes a novel modified RAWIT (RNA amplification with

XX in vitro translation) method, for synthesizing polypeptides encoded by

CC sequences of interest. The method generates a protein from an RNA

CC molecule and comprises (a) incubating the RNA with reverse transcriptase

CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies

CC of the cDNA in the presence of at least 1 oligonucleotide primer which

CC contains an RNA promoter sequence; (c) transcribing the DNA generated

CC with an RNA polymerase to form RNA transcripts; and (d) translating the

CC RNA transcripts in vitro to generate the protein. This sequence encodes a

CC fragment of the murine Factor IX protein which is used to illustrate the

CC RAWTS (RNA amplification with transcript sequencing) method of the

CC invention

XX SQ Sequence 180 BP; 63 A; 29 C; 40 G; 48 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00282 Length: 180

Score: 130.00 Matches: 24

Percent Similarity: 58.33% Conservative: 11

Best Local Similarity: 40.00% Mismatches: 23

Query Match: 10.33% Indels: 2

DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89008 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaLa 40

Db 1 AAGTTGATGATCTCTGTGGAGTGCATCAATTAAGAAATGATGATCTGCTGCC 60

QY 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyClnHisAsnLeuGlnLys 58

Db 61 CACTGTCTTAACCTGCTGATAAATTTGAGTTGTTGCTGCAATATAACATTGATAAG 120

QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78

Db 121 AAGGAAGACACAGAACAAAGGAGAAATGTGATTCCGAACATATCCCTCATCACCAGTACAAT 180

RESULT 29

AAZ89010

ID AAZ89010 standard; DNA; 180 BP.

XX AAZ89010;

AC AAZ89010;

DT 02-JUN-2000 (first entry)

DE Cavea sp. Factor IX DNA fragment.

XX RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;

KW RNA amplification with transcript sequencing; guinea pig; ss.

XX Cavia sp.

OS US6027913-A.

XX 22-FEB-2000.

PD 27-DEC-1994; 94US-00399855.

PF 28-JAN-1988; 88US-00149312.

PR 24-JUL-1989; 89US-00385013.

PR 12-NOV-1993; 93US-00151461.

XX (SOMM/) SOMMER S S.

FA Sommer SS;

XX WPI; 2000-194830/17.

XX P-PSDB; AAY51619.

DR Producing polypeptides from nucleic acid sequences of interest using a

PT modified RAWIT (RNA amplification with in vitro translation) method.

XX Disclosure; Fig 4; 65pp; English.

PS This invention describes a novel modified RAWIT (RNA amplification with

XX in vitro translation) method, for synthesizing polypeptides encoded by

CC sequences of interest. The method generates a protein from an RNA

CC molecule and comprises (a) incubating the RNA with reverse transcriptase

CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies

CC of the cDNA in the presence of at least 1 oligonucleotide primer which

CC contains an RNA promoter sequence; (c) transcribing the DNA generated

CC with an RNA polymerase to form RNA transcripts; and (d) translating the

CC RNA transcripts in vitro to generate the protein. This sequence encodes a

CC fragment of the guinea pig Factor IX protein which is used to illustrate the

CC RAWTS (RNA amplification with transcript sequencing) method of the

CC invention

XX SQ Sequence 180 BP; 64 A; 29 C; 41 G; 46 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00426 Length: 180

Score: 128.00 Matches: 22

Percent Similarity: 61.67% Conservative: 15

Best Local Similarity: 36.67% Mismatches: 21

Query Match: 10.17% Indels: 2

DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89010 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaLa 40

Db 1 GAAACTGAAGCATCTCTGTGGAGTTCATCGTGAATGAAATGCGTAAACAGCTGCC 60

QY 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyClnHisAsnLeuGlnLys 58

Db 61 CACTGTATTCTCCCTGGTATTAAATTTGAGTTGTTCCAGGTAAACATAATATTGAAAG 120

Qy 59 GluGluCysGluGlnThrArgThrAlaThrCluSerPheProHisProGlyPheAsn 78
Db 121 AAGGAAGATACAGAGCAAGCGGAATGTGCACAGATTATTCTGCACCATAGTTACAAT 180
RESULT 30
ABV38446
ID ABV38446 standard; cDNA; 176 BP.
XX AC ABV38446;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 38437.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 7832; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (1) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 176 BP; 29 A; 55 C; 61 G; 31 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.0051 Length: 176
Score: 127.00 Matches: 20
Percent Similarity: 72.22% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 10
Query Match: 10.10% Indels: 0
DB: Gaps: 5
US-09-856-320A-2_COPY_54_282 (1-229) x ABV38446 (1-176)

Qy 6 GluCysGlyPheProHisSerGlnProThrGlnAlaLeuPheCluHisThrArgLeuLeu 25
Db 67 GACTGACGCGGCACTCGCAGCCCTGCGCGGCGCACTGTCATGCGAAACCAATTTGTC 126

Qy 26 CysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHis 41
Db 127 TGCTCGGGCGCTCTGGTGCATCCGCGAGTGGTGCTGTGACGGCGCAC 174
RESULT 31
ABX30380/c
ID ABX30380 standard; cDNA; 169 BP.
XX AC ABX30380;
XX DT 23-APR-2002 (first entry)
XX DE Human G-protein-coupled protease #150.
XX KW Human; ss; gene; G-protein-coupled protease; gene therapy; transgenic;
XX KW protease mediated disorder; proliferative disorder;
XX KW differentiative disorder; developmental disorder;
XX KW haematopoietic disorder.
XX OS Homo sapiens.
XX PN US6331427-B1.
XX PD 18-DEC-2001.
XX PF 26-MAR-1999; 99US-00280116.
XX PR 26-MAR-1999; 99US-00280116.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Robison KE;
XX WPI; 2002-129545/17.
XX New polynucleotides encoding protease homologs of the G-protein-coupled
PT protease family, useful in identifying agonists and antagonists for
PT diagnosis and treatment of protease mediated disorders.
XX Disclosure; Col 185-186; 246pp; English.
XX The invention relates to an isolated human protease nucleic acid molecule
CC comprising a nucleotide sequence of 546 base pairs, one of 268 fully
CC defined in the specification. Also disclosed are production of an
CC isolated polypeptide encoded by the nucleic acid, comprising introducing
CC the nucleic acid into a host cell and culturing under conditions to
CC express the protein from the nucleic acid, use of an antibody to detect
CC the encoded protein in a sample and to modulate its in vivo activity,
CC identifying agents that bind to the protein and identification of a
CC polynucleotide agent that modulates the expression of the nucleic acid or
CC its complement (i.e. gene therapy). The nucleic acid can be used to
CC identify an agent that modulates the expression or activity of the
CC nucleic acid, and can be used to isolate the protein. The nucleic acid
CC can be used in diagnostic assays for determining nucleic acid expression
CC as well as activity in the context of a biological sample (e.g., blood,
CC serum, cells, tissue) to determine whether an individual has a disease or
CC disorder, or is at risk of developing a disease or disorder, associated
CC with aberrant expression or activity of the nucleic acid. The nucleic
CC acid can be used to detect mutations in protease genes and gene
CC expression products such as mRNA. The nucleic acid can be used as
CC hybridisation probes to detect naturally-occurring genetic mutations in a
CC protease gene. The nucleic acid can be used in drug screening methods to
CC identify agonists and antagonists that can be used to diagnose and treat
CC such protease mediated disorders e.g., proliferative, differentiative,
CC developmental or haematopoietic disorders. The nucleic acid can be used
CC as probes, primers, in biological assays, to determine patterns of gene
CC expression, to design ribozymes and to construct transgenic animals. The
CC present sequence represents one of the 268 disclosed human G-protein-
XX coupled protease cDNA sequences
SQ Sequence 169 BP; 40 A; 48 C; 46 G; 35 T; 0 U; 0 Other;
Alignment Scores:

```

Pred. No.: 0.01 Length: 169
Score: 123.50 Matches: 29
Percent Similarity: 56.14% Conservative: 3
Best Local Similarity: 50.88% Mismatches: 24
Query Match: 9.82% Indels: 2
DB: 6 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x ABA92483 (1-169)

QY 157 TyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAsp 176
Db 169 TACCCAGGAGATCACTAAACATCTTCTGCTGGCTTCTGAGGGCGGAAGGAC 110
QY 177 SerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 196
Db 109 TCCGCCCGGGTGACTTTGGTGGCCCTTAGTCTCCAATGGACAACCCCGGGTGTTTT 50
QY 197 SerTyrGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThr 213
Db 49 TCCGGGGGTTATGG----TGTGCCAGAGAGAAACCTGGTTCCACACC 3

RESULT 32
ABA92483
ID ABA92483 standard; DNA; 178 BP.
XX
AC ABA92483;
XX
DT 18-MAR-2002 (first entry)
XX
DE DNA oligonucleotide sequence SEQ ID NO:6.
XX
KW Detection; nucleic acid synthesis; identification; cancer; ss.
XX
OS Synthetic.
XX
PN WO200183817-A1.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-JP003572.
XX
PR 01-MAY-2000; 2000JP-00132667.
XX
PA (BIKE ) EIKEN KAGAKU KK.
XX
PI Mori Y, Nagamine K;
XX
DR WPI; 2002-075170/10.
XX
PT Detecting the product of an enzyme-based nucleic acid synthesizing
PT reaction, useful in gene analysis, diagnosis of cancer and other
PT diseases, and in identifying bacteria, comprises the formation of an
PT insoluble substance.
XX
PS Example 4; Page 18; 44pp; Japanese.
XX
CC The present invention describes a method for detecting the occurrence of
CC a nucleic acid synthesizing reaction during the synthesis of a nucleic
CC acid with an enzyme. The method comprises the use of an insoluble
CC substance formed in the reaction as an indication. The method can be used
CC for detecting the presence or absence of a nucleic acid synthesizing
CC reaction (especially a nucleic acid amplification reaction). The method
CC is useful in gene analysis, diagnosis of cancer and other diseases, and
CC in identifying bacteria. The present sequence represents an
CC oligonucleotide used in the exemplification of the present invention
XX
SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0119 Length: 178
Score: 123.00 Matches: 21
Percent Similarity: 63.46% Conservative: 12
Best Local Similarity: 40.38% Mismatches: 19
Query Match: 9.78% Indels: 0
DB: 6 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABA01120 (1-178)

Query Match: 9.78% Indels: 0
DB: 6 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABA92483 (1-178)

QY 23 ArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuThrAlaAlaHisCys 42
Db 21 AGGGCAGTCTCGGGCGGTTCGTGGTCACCCCGAGTGGTCTTCACAGCTGCCACTGC 80
QY 43 LeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCys 62
Db 81 ATCAGGAACAAAGCGTGATCTTGTGGTCGACACAGCCTGTTTCATCCTGAAGACACA 140
QY 63 GluGlnThrArgThrAlaThrGluSerPheProHis 74
Db 141 GGGCAGGTATTTTCAGTCCAGCCACAGCTTCACACAC 176

RESULT 33
ABA01120
ID ABA01120 standard; DNA; 178 BP.
XX
AC ABA01120;
XX
DT 06-FEB-2002 (first entry)
XX
DE Human PSA nucleotide sequence.
XX
KW Human; nucleic acid synthesis; complementary chain synthesis; diagnosis;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200177317-A1.
XX
PD 18-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-JP002771.
XX
PR 07-APR-2000; 2000JP-00111939.
XX
PA (BIKE ) EIKEN KAGAKU KK.
XX
PI Notomi T, Nagamine K;
XX
DR WPI; 2002-010907/01.
XX
PT Isothermal amplification of nucleic acids using double-stranded nucleic
PT acid as template to establish complementary chain synthesis reaction from
PT primer enabling base pairing in domain to be annealed, useful e.g. in
PT gene diagnosis.
XX
PS Example 1; Page 63; 75pp; Japanese.
XX
CC The invention relates to a method for synthesizing a nucleic acid using a
CC double-stranded nucleic acid as template and incubating under conditions
CC allowing the establishment of a complementary chain synthesis reaction.
CC The method uses an arbitrary primer to initiate the complementary chain
CC synthesis reaction. The method is particularly useful in gene and disease
CC diagnosis. It is a highly efficient and reaction specific method in which
CC no temperature variation is required. The present sequence is used in an
CC example illustrating the invention
XX
SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0119 Length: 178
Score: 123.00 Matches: 21
Percent Similarity: 63.46% Conservative: 12
Best Local Similarity: 40.38% Mismatches: 19
Query Match: 9.78% Indels: 0
DB: 6 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABA01120 (1-178)

```


QY 23 ArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCys 42
DB 21 AGGCGAGTCTGGGGGGTTCCTGTGTCACCCCGAGTGGTCTTCACAGCTGCCACTGC 80
QY 43 LeuLysProArgTyrTlleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCys 62
DB 81 ATCAGGAACAAAAGCGTGTCTTGTGGTGGCAGCCCTGTTTCATCTCTGAAGACACA 140
QY 63 GluGlnThrArgThrAlaThrGluSerPheProHis 74
DB 141 GGCCAGGTATTTTCAGGTGAGCCACAGCTTTCACAC 176
RESULT 34
ID ABS52622 standard; DNA; 178 BP.
AC ABS52622;
XX
XX 15-NOV-2002 (first entry)
XX
XX Human DNA sequence used for polarised light detection.
XX
XX Human; polarised light; detection; amplified nucleic acid product; ds.
XX
XX Homo sapiens.
XX
XX JP2002186481-A.
XX
XX 02-JUL-2002.
XX
XX 18-DEC-2000; 2000JP-00383650.
XX
XX 18-DEC-2000; 2000JP-00383650.
XX
XX (EIKE) EIKEN KAGAKU KK.
XX
XX WPI; 2002-594260/64.
XX
XX Detection method of amplified nucleic acid products with optical
XX
XX Characteristic features using polarized light.
XX
XX Example 1; Page 7; 11pp; Japanese.
XX
XX The present invention relates to the new application of polarised light
XX
XX for detection method of amplified nucleic acid products. The invention
XX
XX can be used for the detection of amplified nucleic acid products. The
XX
XX invention is advantageous as it allows simple detection of amplified
XX
XX nucleic acid products. The present nucleic acid sequence represents a
XX
XX human DNA sequence that was used in the methods of the invention
XX
XX
SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.0119 Length: 178
Score: 123.00 Matches: 21
Percent Similarity: 63.46% Conservative: 12
Best Local Similarity: 40.38% Mismatches: 19
Query Match: 9.78% Indels: 0
DB: 6 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x ABS52622 (1-178)
QY 23 ArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCys 42
DB 21 AGGCGAGTCTGGGGGGTTCCTGTGTCACCCCGAGTGGTCTTCACAGCTGCCACTGC 80
QY 43 LeuLysProArgTyrTlleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCys 62
DB 81 ATCAGGAACAAAAGCGTGTCTTGTGGTGGCAGCCCTGTTTCATCTCTGAAGACACA 140
QY 63 GluGlnThrArgThrAlaThrGluSerPheProHis 74
DB 141 GGCCAGGTATTTTCAGGTGAGCCACAGCTTTCACAC 176

DB 141 GGCCAGGTATTTTCAGGTGAGCCACAGCTTTCACAC 176
RESULT 35
ID ABZ59354
XX 18-APR-2003 standard; DNA; 178 BP.
XX
XX ABZ59354;
XX
XX 15-APR-2003 (first entry)
XX
XX Loop-mediated isothermal amplification related oligonucleotide SEQ.1.
XX
XX Signal reduction; intercalator; gene analysis; disease diagnosis;
XX
XX Loop-mediated isothermal amplification; LAMP; ss.
XX
XX Synthetic.
XX
XX WO2002103053-A1.
XX
XX 27-DEC-2002.
XX
XX 10-JUN-2002; 2002WO-JF005739.
XX
XX 18-JUN-2001; 2001JP-00183716.
XX
XX (EIKE) EIKEN KAGAKU KK.
XX
XX Tomita N, Mori Y;
XX
XX WPI; 2003-175246/17.
XX
XX Method for detecting double-stranded nucleic acids with reduced
XX
XX background noise due to single-stranded nucleic acids, applicable in e.g.
XX
XX gene analysis and disease diagnosis.
XX
XX Example 1; Page 22; 51pp; Japanese.
XX
XX The present invention describes a method for reducing a signal
XX
XX originating from an intercalator bonded to a single-stranded nucleic acid
XX
XX (NA). The method comprises adding a compound reacting preferentially with
XX
XX the intercalator bonded to the single-stranded (NA), in a mixture of the
XX
XX double-stranded (NA) and the single-stranded (NA) to which the
XX
XX intercalator is bonded. Also described: (1) a similar noise-reducing
XX
XX method in which a compound having a higher binding strength to the single
XX
XX -stranded (NA) than the intercalator but a lower binding strength to the
XX
XX double-stranded (NA) than the intercalator bonded to the mixture to reduce such
XX
XX signal originated from the intercalator bonded to the single-stranded
XX
XX (NA); (2) treating the amplification product of a (NA) comprising: (a)
XX
XX amplification of the (NA); adding intercalator to the reaction solution
XX
XX after amplification; reducing signal originating from the intercalator
XX
XX bonded to a single-stranded (NA) by the already- specified method; and
XX
XX measuring fluorescence intensity of the reaction solution; or (b)
XX
XX amplifying the (NA) in the presence of the intercalator; reducing signal
XX
XX from the bond of the intercalator and single-stranded (NA); and measuring
XX
XX fluorescence intensity of the reaction solution; or (c) amplifying the
XX
XX (NA) in the presence of the intercalator and the compound having specific
XX
XX binding strength to the (NA)s, and measuring fluorescence intensity; and
XX
XX (3) kits for detecting double-stranded (NA)s containing the intercalator
XX
XX and any of the specified compounds. The method is applicable in e.g. gene
XX
XX analysis and disease diagnosis. The present sequence represents an
XX
XX oligonucleotide related to loop-mediated isothermal amplification (LAMP),
XX
XX which is used in an example from the present invention
XX
XX
SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.0119 Length: 178
Score: 123.00 Matches: 21
Percent Similarity: 63.46% Conservative: 12
Best Local Similarity: 40.38% Mismatches: 19
Query Match: 9.78% Indels: 0
DB: 7 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABZ59354 (1-178)

QY 23 ArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCys 42
 Db 21 AGGCGAGTCTCGCGGGTGTCTGTGTCACCCCGAGTGGTCTTCACAGCTGCCACTGC 80
 QY 43 LeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCys 62
 Db 81 ATCAGGACAAACGCGATCTCTGGTGGCGACAGCTGTTCATCTCTGAGACACA 140
 QY 63 GluGlnThrArgThrAlaThrGluSerPheProHis 74
 Db 141 GCCCAGGTAATTCAGGTCAGCCACAGCTTCACACAC 176

RESULT 36

AAZ89012
 ID AAZ89012 standard; DNA; 180 BP.

XX AC AAZ89012;

XX DT 02-JUN-2000 (first entry)

XX DE Sheep Factor IX DNA fragment.

XX KW RAWIT; RNA amplification with in vitro translation; RAWITS; Factor IX;
 XX RNA amplification with transcript sequencing; sheep; ss.

XX OS Ovis sp.

XX PN US6027913-A.

XX PD 22-FEB-2000.

XX PF 27-DEC-1994; 94US-00399855.

XX PR 28-JAN-1988; 88US-00149312.

XX PR 24-JUL-1989; 89US-00385013.

XX PR 12-NOV-1993; 93US-00151461.

XX PA (SOMM/) SOMMER S S.

XX PI Sommer SS;

XX DR WPI; 2000-194830/17.

XX DR P-FSDB; AAY51622.

XX PT Producing polypeptides from nucleic acid sequences of interest using a
 modified RAWIT (RNA amplification with in vitro translation) method.

XX PS Disclosure; Fig 4; 65pp; English.

XX CC This invention describes a novel modified RAWIT (RNA amplification with
 in vitro translation) method, for synthesizing polypeptides encoded by
 sequences of interest. The method generates a protein from an RNA
 molecule and comprises (a) incubating the RNA with reverse transcriptase
 to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies
 of the cDNA in the presence of at least 1 oligonucleotide primer which
 contains an RNA promoter sequence; (c) transcribing the DNA generated
 with an RNA polymerase to form RNA transcripts; and (d) translating the
 RNA transcripts in vitro to generate the protein. This sequence encodes a
 fragment of the sheep Factor IX protein which is used to illustrate the
 CC RAWITS (RNA amplification with transcript sequencing) method of the
 CC invention

SQ Sequence 180 BP; 64 A; 29 C; 39 G; 48 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0182 Length: 180
 Score: 121.00 Matches: 22
 Percent Similarity: 56.67% Conservative: 12
 Best Local Similarity: 36.67% Mismatches: 24
 Query Match: 9.62% Indels: 2
 DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89012 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
 Db 1 AAAGTTGAGGCGTCTCTGTGGAGGTTCTATCATTAATGAAAAATGGTCGTAACTCGAGCC 60

QY 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 58
 Db 61 CACTGTATCAAAACCGGATGATAATATTACAGTTCTTGCAAGTGAATATAACATTTCAGGAG 120

QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78
 Db 121 ACTGGAATACAGAGCAAGGAAATGTGATTTCGTAATTATTCCTTACCACAAATACAA 180

RESULT 37

ABV38147/c

ID ABV38147 standard; cDNA; 179 BP.

XX AC ABV38147;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 38138.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of
 prostate cells and correlating with presence of prostate cancer, useful
 for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 7788; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
 a nucleotide sequence given in tables 1-9 (ABV00010-ABV62213) of the
 specification or its complement. (I) is useful for: (a) assessing whether
 a patient is afflicted with prostate cancer; (b) monitoring the
 progression of prostate cancer in a patient; (c) assessing the efficacy
 of a test compound to inhibit prostate cancer in a patient; (d) assessing
 the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

SQ Sequence 179 BP; 37 A; 51 C; 55 G; 36 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0201 Length: 179
 Score: 120.50 Matches: 21

Percent Similarity: 62.79% Conservative: 6
Best Local Similarity: 48.84% Mismatches: 9
Query Match: 9.58% Indels: 7
DB: 5 Gaps: 1

US-09-856-320a-2_COPY_54_282 (1-229) x ABV38147 (1-179)

Qy 183 GlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspPro 202
Db 179 GGGGGCCCACTTGTCTGTATGCTGCTTCAGGTATACAGTCATCGGGCAGTGAACCA 120

Qy 203 CysAlaIleThrArgLysProGlyValThr-----LysVal 215
Db 119 TGTGCCCTGCCGAAAGGCCTTCCTGTACTCGCGCGACACGCTAAGGGCGGAATTC 60

Qy 216 CysLysTyr 218
Db 59 TGCAGATAT 51

RESULT 38
ABV44351/c

ID ABV44351 standard; cDNA; 179 BP.

XX AC ABV44351;

DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 44342.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW Pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX FN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 25-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JB;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of

XX PT prostate cells and correlating with presence of prostate cancer, useful

XX PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 8804; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising

XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

XX CC specification or its complement. (I) is useful for: (a) assessing whether

XX CC a patient is afflicted with prostate cancer; (b) monitoring the

XX CC progression of prostate cancer in a patient; (c) assessing the efficacy

XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing

XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;

XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;

XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)

XX CC determining whether prostate cancer has metastasized in a patient; (h)

XX CC assessing the aggressiveness or indolence of prostate cancer in a patient

XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 179 BP; 37 A; 51 C; 55 G; 36 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0201 Length: 179
Score: 120.50 Matches: 21
Percent Similarity: 62.79% Conservative: 6
Best Local Similarity: 48.84% Mismatches: 9
Query Match: 9.58% Indels: 7
DB: 5 Gaps: 1

US-09-856-320a-2_COPY_54_282 (1-229) x ABV44351 (1-179)

Qy 183 GlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspPro 202

Db 179 GGGGGCCCACTTGTCTGTATGCTGCTTCAGGTATACAGTCATCGGGCAGTGAACCA 120

Qy 203 CysAlaIleThrArgLysProGlyValThr-----LysVal 215
Db 119 TGTGCCCTGCCGAAAGGCCTTCCTGTACTCGCGCGACACGCTAAGGGCGGAATTC 60

Qy 216 CysLysTyr 218
Db 59 TGCAGATAT 51

RESULT 39
AAD58752

ID AAD58752 standard; DNA; 172 BP.

XX AC AAD58752;

DT 04-DEC-2003 (first entry)

XX DE Human transmembrane serine protease (TSP1-TSP34) gene exon 7.

XX KW Human; transmembrane serine protease; TSP; therapy; immunogen; cancer;

XX KW autoimmune disease; immunomodulatory; immunosuppressive; enzyme; ds.

XX OS Homo sapiens.

XX FN WO2003064641-A1.

XX PD 07-AUG-2003.

XX PF 24-JAN-2003; 2003WO-EP000756.

XX PR 30-JAN-2002; 2002US-0352806P.

XX PA (GENE-) GENEPROT INC.

XX PI Bougueleret L, Niknejad A, Saudrais C;

XX DR WPI; 2003-627608/59.

XX PT New purified transmembrane serine protease polypeptides (TSP1-TSP34)

XX PT comprising a protease domain or its biologically active portion, useful

XX PT for identifying modulators of proteolysis.

XX PS Claim 6; Page 229; 276pp; English.

XX CC The invention relates to purified human transmembrane serine protease

XX CC (TSP) polypeptide, comprising a protease domain of a type-II membrane-

XX CC type serine protease or its biologically active portion. The invention is

XX CC useful for cleaving a TSP substrate protein by contacting TSP with a

XX CC substrate protein under serine protease activity permissive conditions.

XX CC The invention is useful as an immunogen to generate antibodies that bind

XX CC TSP or TSP1-TSP43 proteins, useful for treating disease e.g. cancer and

XX CC autoimmune disease. The present sequence is human TSP1-TSP34 gene exon

XX SQ Sequence 172 BP; 31 A; 46 C; 61 G; 34 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0395 Length: 172
Score: 117.00 Matches: 21
Percent Similarity: 61.90% Conservative: 5

Best Local Similarity: 50.00% Mismatches: 16
 Query Match: 9.30% Indels: 0
 DB: 8 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x AAD58752 (1-172)

Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
 Db 39 ATCTGGCGCGCATGGAAGCATCCCGGGGAGTTCCTGGCGCAAGCCCTTCGAGAG 98
 Qy 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
 Db 99 AACAGAGACATCTCTGTGGGGCGCCATCAAGCCAGGTGGTGGTGTCTGTCTGT 158
 Qy 41 HisCys 42
 Db 159 CACTGC 164

RESULT 40

AAZ89007
 ID AAZ89007 standard; DNA; 180 BP.

XX AC AAZ89007;

DT 02-JUN-2000 (first entry)

DE Human Factor IX DNA fragment.

XX KW RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;
 KW RNA amplification with transcript sequencing; human; ss.

XX OS Homo sapiens.

XX FN US6027913-A.

XX PD 22-FEB-2000.

XX PF 27-DEC-1994; 94US-00399855.

XX PR 28-JAN-1988; 88US-00143112.

XX PR 24-JUL-1989; 89US-00385013.

XX PR 12-NOV-1993; 93US-00151461.

XX PA (SOMM/) SOMMER S S.

XX PI Sommer SS;

XX DR WPI; 2000-194830/17.

XX DR P-PSDB; AAY51617.

XX PT Producing polypeptides from nucleic acid sequences of interest using a
 PT modified RAWIT (RNA amplification with in vitro translation) method.

XX PS Disclosure; Fig 4; 65pp; English.

XX CC This invention describes a novel modified RAWIT (RNA amplification with
 CC in vitro translation) method, for synthesizing polypeptides encoded by
 CC sequences of interest. The method generates a protein from an RNA
 CC molecule and comprises (a) incubating the RNA with reverse transcriptase
 CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies
 CC of the cDNA in the presence of at least 1 oligonucleotide primer which
 CC contains an RNA promoter sequence; (c) transcribing the DNA generated
 CC with an RNA polymerase to form RNA transcripts; and (d) translating the
 CC RNA transcripts in vitro to generate the protein. This sequence encodes a
 CC fragment of the human Factor IX protein which is used to illustrate the
 CC RAWTS (RNA amplification with transcript sequencing) method of the
 CC invention

SQ Sequence 180 BP; 62 A; 30 C; 39 G; 49 T; 0 U; 0 Other;

Alignment Scores: 0.0419 Length: 180
 Pred. No.: 117.00 Matches: 20
 Score:

Percent Similarity: 56.67% Conservative: 14
 Best Local Similarity: 33.33% Mismatches: 24
 Query Match: 9.30% Indels: 2
 DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89007 (1-180)

Qy 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
 Db 1 AAAGTTGATGATCTCTGTGGAGGCTCTATCGTTAATGAAAAATGATGTAACCTGCTGCC 60
 Qy 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 58
 Db 61 CACTGTGTGTTAAACTGTGTTAAATTAACACTTTCGCGAGTGAACATAATATTGAGGAG 120
 Qy 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78
 Db 121 ACAGAACATACAGAGCAAAAGCGAAATGTGATTGGAATTATTCCTCACCACACTACAT 180

RESULT 41

AAZ89007

ID AAZ89007 standard; DNA; 172 BP.

XX AC AAZ89007;

DT 04-DEC-2003 (first entry)

DE Human transmembrane serine protease (TSP1-TSP34) gene exon 11.

XX KW Human; transmembrane serine protease; TSP; therapy; immunogen; cancer;
 KW autoimmune disease; immunomodulatory; immunosuppressive; enzyme; ds.

XX OS Homo sapiens.

XX FN WO2003064641-A1.

XX PD 07-AUG-2003.

XX PF 24-JAN-2003; 2003WO-EP000756.

XX PR 30-JAN-2002; 2002US-0352806P.

XX PA (GENE-) GENEPROT INC.

XX PI Bougueleret L, Niknejad A, Saudrais C;

XX DR WPI; 2003-627608/59.

XX PT New purified transmembrane serine protease polypeptides (TSP1-TSP34)
 PT comprising a protease domain or its biologically active portion, useful
 PT for identifying modulators of proteolysis.

XX PS Claim 6; Page 232; 276pp; English.

XX CC The invention relates to purified human transmembrane serine protease
 CC (TSP) polypeptide, comprising a protease domain of a type-II membrane-
 CC type serine protease or its biologically active portion. The invention is
 CC useful for cleaving a TSP substrate protein by contacting TSP with a
 CC substrate protein under serine protease activity permissive conditions.
 CC The invention is useful as an immunogen to generate antibodies that bind
 CC TSP or TSP1-TSP34 proteins, useful for treating disease e.g. cancer and
 CC autoimmune disease. The present sequence is human TSP1-TSP34 gene exon
 XX Sequence 172 BP; 26 A; 51 C; 66 G; 29 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0486 Length: 172
 Score: 116.00 Matches: 20
 Percent Similarity: 64.29% Conservative: 7
 Best Local Similarity: 47.62% Mismatches: 15
 Query Match: 9.22% Indels: 0
 DB: 8 Gaps: 0

QY 195 llelleSerTrpGlyGlnAspProCysAlaIalleThrArgLysProGlyValTyThrLys 214
 DB 61 ATTGAAGCTGGGA--GATAACTGTGGTCAAAAGGACACGCTGGAGTCTACACAA 117
 QY 215 ValCysLysTyValAspTrpIle 222
 DB 118 GTGACTTATTACCGAAACTGGATT 141
 RESULT 44
 AAK21293
 ID AAK21293 standard; DNA; 162 BP.
 XX
 AC AAK21293;
 DT 05-NOV-2001 (first entry)
 DE Human brain expressed single exon probe SEQ ID NO: 21284.
 XX
 KW Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US0000667.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483446/52.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 XX
 PS Example 4; SEQ ID NO 21284; 650pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention
 XX
 SQ Sequence 162 BP; 51 A; 28 C; 43 G; 40 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.0554 Length: 162
 Score: 115.00 Matches: 26
 Percent Similarity: 60.42% Conservative: 3
 Best Local Similarity: 54.17% Mismatches: 13
 Query Match: 9.14% Indels: 6
 DB: 4 Gaps: 2
 US-09-856-320A-2_COPY_54_282 (1-229) x AAK21293 (1-162)
 QY 180 GlyAspSerGlyGlyProLeuValCysAsnGln-----SerLeuGlnGly 194
 DB 1 GGTGATTCTGGGGGACCTTTAGTACCAAGGATCGTAAGATACGCTGGTATCTCATTTGGA 60

QY 195 llelleSerTrpGlyGlnAspProCysAlaIalleThrArgLysProGlyValTyThrLys 214
 DB 61 ATTGAAGCTGGGA--GATAACTGTGGTCAAAAGGACACGCTGGAGTCTACACAA 117
 QY 215 ValCysLysTyValAspTrpIle 222
 DB 118 GTGACTTATTACCGAAACTGGATT 141
 RESULT 45
 ABS47188
 ID ABS47188 standard; DNA; 162 BP.
 XX
 AC ABS47188;
 DT 25-FEB-2003 (first entry)
 DE Human liver single exon probe, SEQ ID No 22178.
 XX
 KW Human; single exon nucleic acid probe; liver; cirrhosis;
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW coronary heart disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157273-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US0000664.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488898/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX
 PS Claim 4; SEQ ID NO 22178; 658pp; English.
 XX
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human
 CC liver single exon nucleic acid probes of the invention. Note: The
 CC sequence information for this patent does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 162 BP; 51 A; 28 C; 43 G; 40 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.0554 Length: 162
 Score: 115.00 Matches: 26
 Percent Similarity: 60.42% Conservative: 3
 Best Local Similarity: 54.17% Mismatches: 13
 Query Match: 9.14% Indels: 6

DB: 4 Gaps: 2
US-09-856-320A-2_COPY_54_282 (1-229) x ABS47188 (1-162)
QY 180 GLVAspSerGlyGlyProLeuValCysAsnGln-----SerLeuGlnGly 194
Db 1 GGTGATCTGGGGACCTTTAGTTCACAGGATCTGAAGATACGTGGTATCATTTGGA 60
QY 195 IleleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyThrLys 214
Db 61 ATTGTAACTGGGA--GATAACTGTGTGTTCAAAAGGACACAGCTGGAGTGTACACAA 117
QY 215 ValCysLysTyrrValAspTrpIle 222
Db 118 GTGACTTATTACCGAAACTGGATT 141
RESULT 46
ID ABV97886/c
ID ABV97886 standard; cDNA; 184 BP.
XX ABV97886;
AC
XX
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 3294.
XX
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytotstatic; tumour; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200260317-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 30-JAN-2002; 2002WO-US002781.
PF
XX
XX 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI
XX WPI; 2002-627435/67.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
XX Claim 1; SEQ ID NO 3294; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene

CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIFO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 184 BP; 41 A; 59 C; 53 G; 31 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.0803 Length: 184
Score: 114.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 9.06% Indels: 6
DB: Gaps: 3
US-09-856-320A-2_COPY_54_282 (1-229) x ABV97886 (1-184)
QY 1 IlelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---Phe 19
Db 178 GTTGTCAATGGTGAGGATCGGTCCCTACAGTGGCCCTGGCAGGTTTCCCTGCAGTAT 119
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 118 GAGAAAGTGAAGCTTCTACACACGTGTGGGGTAGCTCATCGCCCGCAGTGGTT 59
QY 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrrIleValHisLeuGlyGln 53
Db 58 GTGACTGCCGGCCACTGCATCTCGAGTCTCTCGAGCTCTCGAGTGTGTGGCGCGAG 2
RESULT 47
ABV98082
ID ABV98082 standard; cDNA; 195 BP.
XX
XX ABV98082;
AC
XX
XX 14-JAN-2003 (first entry)
DT
XX
XX Human pancreatic cancer expressed cDNA SEQ ID NO 3490.
DE
XX
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytotstatic; tumour; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200260317-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 30-JAN-2002; 2002WO-US002781.
PF
XX
XX 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI
XX WPI; 2002-627435/67.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
XX Claim 1; SEQ ID NO 3490; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene

CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 195 BP; 31 A; 59 C; 60 G; 45 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.0864 Length: 195
 Score: 114.00 Matches: 24
 Percent Similarity: 61.02% Conservative: 12
 Best Local Similarity: 40.68% Mismatches: 17
 Query Match: 9.06% Indels: 6
 DB: Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x ABV98082 (1-195)

QY 1 IlelelysglypHeGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
 Db 18 GTTGTCAATGGTGAGGATCGGTCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 77
 QY 20 GlutylsThrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
 Db 78 GAGAAAGTGGAGCTTCTACACAGCTGGCGGGTAGCTCTATCGCCCGGACTGGGTT 137
 QY 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
 Db 138 GTGACTGCGCGCCACTGCTATCTCGAGCTCTCGACCTCGACCTACAGGTGGTGTGGTGAG 194

RESULT 48
 ABV98457
 ID ABV98457 standard; cDNA; 214 BP.
 XX AC ABV98457;
 XX DT 14-JAN-2003 (first entry)
 XX DE Human pancreatic cancer expressed cDNA SEQ ID NO 3865.
 XX KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
 XX KW cytosolic; tumour; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200260317-A2.
 XX PD 08-AUG-2002.
 XX PF 30-JAN-2002; 2002WO-US002781.
 XX PR 30-JAN-2001; 2001US-0265305P.
 XX PR 31-JAN-2001; 2001US-0265682P.
 XX PR 09-FEB-2001; 2001US-0267568P.
 XX PR 21-MAR-2001; 2001US-0278651P.
 XX PR 28-APR-2001; 2001US-0287112P.
 XX PR 16-MAY-2001; 2001US-0291631P.
 XX PR 12-JUL-2001; 2001US-0305484P.
 XX PR 20-AUG-2001; 2001US-0313999P.
 XX PR 27-NOV-2001; 2001US-0333626P.
 XX PA (CORI-) CORIXA CORP.

PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX WPI; 2002-627435/67.
 XX PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 XX diagnosing, preventing and/or treating cancer, particularly pancreatic
 XX cancer.
 XX PS Claim 1; SEQ ID NO 3865; 300pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV9428-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 214 BP; 33 A; 68 C; 64 G; 49 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.0973 Length: 214
 Score: 114.00 Matches: 24
 Percent Similarity: 61.02% Conservative: 12
 Best Local Similarity: 40.68% Mismatches: 17
 Query Match: 9.06% Indels: 6
 DB: Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x ABV98457 (1-214)

QY 1 IlelelysglypHeGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
 Db 37 GTTGTCAATGGTGAGGATCGGTCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 96
 QY 20 GlutylsThrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
 Db 97 GAGAAAGTGGAGCTTCTACACAGCTGGCGGGTAGCTCTATCGCCCGGACTGGGTT 156
 QY 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
 Db 157 GTGACTGCGCGCCACTGCTATCTCGAGCTCTCGACCTACAGGTGGTGTGGTGAG 213

RESULT 49
 AAA64312/C
 ID AAA64312 standard; DNA; 94 BP.
 XX AC AAA64312;
 XX DT 20-DEC-2000 (first entry)
 XX DE PCR primer for a protein C activator polypeptide DNA fragment.
 XX KW Protein C activator; PCA; venom; snake; blood coagulation; factor VIIa;
 XX KW activated protein C; APC; anticoagulant; Factor Va; clot formation;
 XX KW trypsin-type serine protease; blood coagulation factor; PCR primer; ss.
 XX OS Agkistrodon contortrix contortrix.
 XX PN WO200050612-A2.
 XX PD 31-AUG-2000.
 XX PF 22-FEB-2000; 2000WO-US004406.


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XX 22-FEB-1999; 99US-0121121P.
XX (INLI ) INSTRUMENTATION LAB.
XX Kunes YZ, Sanz M, Tumanova IA, Birr CA, Shi PQ, Bruguera P;
XX Ruiz JA, Sanchez-Martinez D;
XX WPI; 2000-543915/49.
XX
XX Pure protein C activator (PCA) preparation comprising a PCA protein with
XX a defined sequence found in Agkistrodon contortrix conortrix (ACC)
XX venom, useful for evaluating the level or activity of blood coagulation
XX factors.
XX Example; Page 46; 47pp; English.
XX
XX PCR primers AAA64311-14 were used to amplify a fragment of DNA encoding a
XX protein C activator (PCA). The polypeptide is found in the venom of the
XX snake Agkistrodon contortrix conortrix. PCA is an enzyme in the blood
XX coagulation pathway that is normally activated by a complex series of
XX events to become activated protein C (APC). APC has an anticoagulant
XX effect by inactivating Factors Va and VIIIa, and thereby slowing the
XX conversion of fibrinogen to fibrin and clot formation. The PCA of the
XX invention is a trypsin-type serine protease. The PCA protein is useful in
XX diagnostic kits for evaluating the level or activity of blood coagulation
XX factors
XX
XX Sequence 94 BP; 28 A; 20 C; 21 G; 25 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.042 Length: 94
XX Score: 113.00 Matches: 20
XX Percent Similarity: 77.42% Conservative: 4
XX Best Local Similarity: 64.52% Mismatches: 7
XX Query Match: 8.98% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-856-320A-2_COPY_54_282 (1-229) x AAA64312 (1-94)
XX
XX QY 185 ProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAla 204
XX Db 93 CCATTGATCTGTAAACGGTCAATTCGAAGGTATCTGCTGTTGGTGAACCCATGTGCT 34
XX
XX QY 205 IleThrArgLysProGlyValTyrThrLysVal 215
XX Db 33 CAACCAAGAAAGCCAGGTAATACATAAGTT 1
XX
XX RESULT 50
XX ABV98446/c
XX ID ABV98446 standard; cDNA; 205 BP.
XX
XX AC ABV98446;
XX
XX DT 14-JAN-2003 (first entry)
XX
XX DE Human pancreatic cancer expressed cDNA SEQ ID NO 3854.
XX
XX KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX cytostatic; tumour; gene, ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200260317-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 30-JAN-2002; 2002WO-US002781.
XX
XX PR 30-JAN-2001; 2001US-0265305P.
XX PR 31-JAN-2001; 2001US-0265682P.
XX PR 09-FEB-2001; 2001US-0267568P.
XX PR 21-MAR-2001; 2001US-0278651P.
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PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
XX
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosing, preventing and/or treating cancer, particularly pancreatic
XX cancer.
XX
XX Claim 1; SEQ ID NO 3854; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a), under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridization, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene
XX therapy. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 205 BP; 49 A; 61 C; 61 G; 33 T; 0 U; 1 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.113 Length: 205
XX Score: 113.00 Matches: 24
XX Percent Similarity: 61.02% Conservative: 12
XX Best Local Similarity: 40.68% Mismatches: 17
XX Query Match: 8.98% Indels: 6
XX DB: 6 Gaps: 3
XX
XX US-09-856-320A-2_COPY_54_282 (1-229) x ABV98446 (1-205)
XX
XX QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
XX Db 178 GTTGTCATGCTGAGGATGGGTCCCTACAGCTGGCCCTGGCAGGTTCCCTGCAGTAT 119
XX
XX QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
XX Db 118 CAGAAAAGTGGAGCTTCTACACANGTGTGGGGTAGCCTCATCGCCCGCGATTGGTT 59
XX
XX QY 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
XX Db 58 GTGATCCCGCCCACTGCATCTCGAGGGATCTGACCTACCAGGTTGTTGGTGGAG 2
XX
XX Search completed: June 27, 2004, 00:25:32
XX Job time : 476 secs
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